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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:
July 1, 2002, 06:16:18; Search time 49.45 Seconds
(without alignments)
40.806 Million cell updates/sec
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Scoring table: HLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

91.7 91.7 91.7 91.7 91.7 92.8 93.8 94.7 95.8 97.7 96.8 97.7 96.8 97.9 98.8 97.9 98.8 97.9 98.8 97.9 98.8 97.9 98.8 97.9 98.8	ם לה ו		91.7 21	91.7 38	91.7 51	03 95 3 16	93 85.3 16	90 82.6 48	87 79.8 10	31.0	84 //.1	81 74.3	80 73.4	78 71.6	78 71.6	78 71.6	77 70.6	77 70.6	77 70.6	76 69.7	76 69.7	75 68.8	75 68.8	74 67.9	74 67.9	74 67.9	74 67 9		73 67.0	73 67.0 72.5 66.5	73 67.0 72.5 66.5 72 66.1	73 67.0 72.5 66.5 72 66.1 72 66.1	73 67.0 72.5 66.5 72 66.1 72 66.1 72 66.1 72 66.1
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T46395 T46395 T18513 T18513 F71619 C86477 A484455 T18452 T18452 T163699 T163699 T1627219 A86288 T16288 T18427 T184	ID		52	39	17	י ב	5	61	47		A48455	T18440	T18452	T50609	T06377	T42727	JC7219	A86288	T18427	\$58322	\$43604	T38485	\$48550	T23594	D97301	F64386	UΠ	U	$\sim$	Φ	œ	_	
hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote protein F1504.29 [ acidic phosphoprot hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote of hypothetical protein SAR DNA-binding proliferation pote proliferation pote nuclear protein F9L1.30 [i hypothetical protein R07E5.1 protein R07E5.1 protein (centromere/microtumypothetical protein hypothetical protein hypothetical protein probable membrane hypothetical p	cription	******************	Ñ	۰,	-,	٠,	-	_	1001				_	- '	DNA-bindi	i forst ion	niic lear protein	5011		leolar prote	ביי קייטרט	TO THE STANFORT THE COLUMN	hynothetical ar		probable membra	hypothetical pr	m i	related to proline	obable pr	3.	2 ,	2 6	

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2 KKKKKKKKKKKKKKKKKKKK 21

Query Match 91.7%; Score 100; DB 2; Length 380; Best Local Similarity 100.0%; Pred. No. 0.0025; Matches 20; Conservative 0; Mismatches 0; Indels

0

Gaps

0;

# ALIGNMENTS

RESULT 2 T46395 hypothetical protein DKFZp434I1120.1 - human (fragment) C:Species: Homo sapiens (man) C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 C:Accession: T46395 R:Ottenwaelder, B:: Obermaier, B:: Mewes, H.W:: Gassenhuber, J:: Wiemann, S. Submitted to the Protein Sequence Database, January 2000 A:Reference number: Z23031 A:Accession: T46395 A:Status: preliminary A:MOlecule type: mRNA A:Residues: 1-380 <aaa> A:Cross-references: EWBL:AL137556 A:Experimental source: adult testis; clone DKFZp434I1120 C:Genetics: A:Note: DKFZp434I1120.1</aaa>	Query Match 91.7%; Score 100; DB 2; Length 215; Best Local Similarity 100.0%; Pred. No. 0.0017; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 2 KKKKKKKKKKKKKKKKK 21 Db 35 KKKKKKKKKKKKKKKK 54	R;Wang, Z.Q.; Akmal, K.M.; Kim, K.H. Biol. Reprod. 51, 1022-1030, 1994 A;Title: An unusual nucleoporin-related messenger ribonucleic acid is present A;Reference number: 152523; MUID:95151924 A;Accession: 152523 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-215 <res> A;Residues: 1-215 <res> A;Cross-references: GB:575997; NID:9913245; PIDN:AAB33384.1; PID:9913246 A;Experimental source: testis</res></res>	RESULT 1 152523 nucleoporin p62 homolog - rat (fragment) C:Species: Rattus norvegicus (Norway rat) C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 05-Nov-1999 C:Accession: 155523
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355

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R;Gardner, M.J.; Tettelin, H.; Pertea, M.; Salzberg, S.; Scienc; 282, 1126-1132, 1998
                                                                             hypothetical protein PFB0235w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 C;Accession: F71619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T18513
hypothetical protein C0845c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T18513
R;Lawson, D.; Bowman, S.; Barrell, B.
                                                                                                                                                           RESULT
F71619
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A;Introns: 312/3; 359/3;
C;Superfamily: Arabidopsi
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A; Introns: 19/1
A; Note: C0845c
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A; Residues: 1-166 <LAW>
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A;Experimental source: cultivar Columbia; BAC clone T20N10
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A; Residues: 1-517 <DAN>
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A;Accession: T49173
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R:D'Angelo, M.; Vezzi, A.: Modesto,
       A; Title:
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Arabidopsis thaliana hypothetical protein F17J16.30
                                     Tettelin, H.; Carucci, D.J.; Cummings, L.M.; alzberg, S.; Zhou, L.; Sutton, G.G.; Clayton,
                                                                                                                                                                                                                                                                                                              Conservative
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     sequence of the
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90.0%;
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Sequence Database, April 2000
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   human malaria
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Plasmodium falciparum.
                                   Aravind, L.; Koonin, R.; White, O.; Smith,
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R:Deleersnijder, W.; Prasomsitti, P.; Tungpradubkul, S.; Hendrix, D.; Hamers-Casterme Mol. Biochem. Parasitol. 56, 59-68, 1992
A;Title: Structure fa Plasmodium chabaudi acidic phosphoprotein that is associated A;Reference number: A48455; MUID:93116806
A;Accession: A48455
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Maizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: C86477
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C86477
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor
C;Accession: C86477
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
     A;Cross-references: GB:M95789; NID:g160602; PID:g160603
A;Experimental source: IP-PC1/C
A;Note: sequence extracted from NCBI backbone (NCBIN:12
                                                                                                                                                                                                                                                                                                        acidic phosphoprotein PcEMAlq - Plasmodium chabaudi
C;Species: Plasmodium chabaudi
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
                                                                                A; Molecule type: nucleic acid
A; Residues: 1-441 <DEL>
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A; Residues: 1-107 <S'
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94.4%;
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NCBI backbone (NCBIN:121415,
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1; Mismatches
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R.; Marzia
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RESULT
T50609
     hypothetical protein DKFZp761B2423.1 - C:Species: Homo sapiens (man) C:Date: 21-Jul-2000 #sequence_revision
                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-784 <LAW>
A; Cross-references: EMB
                                                                                                           В
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                                                                                                                                                                                                                                     A; Map position:
A; Note: C0560c
                                                                                                                                                                                                                                                                                                                                                            R:Lawson, D.; Bowman, S.; Barrell, B. submitted to the EMBL Data Library, November 1998
                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C0560c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jun-2000
C:Accession: T18452
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T18452
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T18440
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A; Accession: T18452
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A;Residues: 1-4550 <LAW>
A;Cross-references: EMBL:298547; NID:el325376; PID:el325396; PIDN:CAB11121.1
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note:
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                                                                                                                                                                 Query Match
Best Local S
Matches 15
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Best Local S
Matches 19
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Best Local
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                                                                                                        360 EKKKKQKKKKQKKKQKKKQ 379
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                                                                                                                                                                Local Similarity hes 15; Conserv
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19; Conserv
                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.38;
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80.08;
                                                                                                                                                                             73.48;
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                                                                                                                                                                             Score 80; DB 2; Pred. No. 0.31;
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Pred. No. 0.
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                                                                                                                                                                Mismatches
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21-Jul-2000 #text_change 21-Jul-2000
                                human (fragment)
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0.77;
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0.089;
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R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Wei
submitted to the Protein Sequence Database, June 2000
A;Reference number: Z25143
A;Accession: T50609
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-529 <AAA>
A;Cross-references: EMBL:AL359564
A;Experimental source: adult amygdala; clone DKFZp761B242:
C;Genetics:
A:Description: involved in hnrNP association C:Superfamily: RING finger homology F:57-107/Domain: RING finger homology <RRN>
                                                                                                                       A:Status: preliminary: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1560 <NIT>
A:Cross-references: EMBL:U83913; NID:g3858884; PID:g3858885; PIDN:AAC72432.1
A:Experimental source: strain Balb/C
A:Experimental source: strain Balb/C
                                                                                                                                                                                                                                                                                    proliferation potential-related protein - mouse C;Species: Mus musculus (house mouse) C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change C;Accession: T42727 R;Witte, M.M.; Scott, R.E.
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T42727
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A; Accession: T42727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Hatton, D.; Gray, J.C.
submitted to the EMBL Data Library, April 1998
A;Description: cDNA encoding a pea SAR DNA-binding protein that shows homology to A;Reference number: Z15637
A;Accession: T06377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAR DNA-binding protein-1 - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 30-Apr-1999 *sequence_revision 30-Apr-1999 *text_change 02-Jun-2000
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                                                                       C; Function:
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                                                                                                          C; Genetics:
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Best Local Similarity 80.0
Matches 16; Conservative
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Best Local :
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15; Conserv
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, Data Library, November 1998
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80.0%;
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75.08;
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Pred. No.
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Pred. No.
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0.38;
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                                         Rb1 binding
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protein F9L1.30 [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Accession: A86288
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Anseen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A. Accession: A86288
A. Status, A. Salzberg, C. Salzberg, C.
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                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE005172; NID:g5103832; PIDN:AAD39662.1; GSPDB:GN00141
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A; Residues: 1-266 <STO>
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A;Residues: 1-229 <SAS>
A;Cross-references: DDBJ.AB035383; NID:g7619895; PIDN:BAA94743.1; PID:g7619896
A;Experimental source: MIN6 cell line
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Biochem. Biophys. Res. Commun. 269, 444-450, 2000
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C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C;Accession: JC7219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nuclear protein SR-25 - mouse
                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                      Best Local Similarity 70.0
Matches 14; Conservative
                                                                                                                                                                                     Query Match
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Best Local Similarity 75.0%;
Matches 15; Conservative
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Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                               position:
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95 KHKEKKRKKKKKKKKKKKKKKK 114
2 KKKKKKKKKKKKKKKKKKKK 21
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                                                                                                                                        70.6%;
70.0%;
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Pred. No. 0.74;
1; Mismatches
                                                                                                                                        Score 77; [
Pred. No. 0.
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Pred. No. 0.27;
                                                                                                         Mismatches
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231 KRKKRRKNKKKKNKKEKKKK 250
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R; Lawson, D.; Bowman, S.; Barreil, E submitted to the EMBL Data Library, A; Reference number: 218935
A; Accession: T18427
A; Accession: T18427 C; Genetics: A; Introns: 307/1; 1545/2 A; Note: C0335c A;Molecule type: DNA A;Residues: 1-3724 <LAW> A;Cross-references: EMBL:298547; NID:e1325376; PID:e1325379; PIDN:CAB11104.1 hypothetical protein C0335c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jun-2000 A;Status: preliminary; translated from GB/EMBL/DDBJ C; Accession: T18427 , B. :y, August 1997

Query Match Best Local S Matches 15 2201 CEIKKKMKRKKKMKKKKKKK Local Similarity 75.0 hes 15; Conservative 1 CKKKKKKKKKKKKKKKKKKK 20 70.68; 2220 ν, Score 77; Pred. No. Mismatches DB 1.6; 2; Length 3724; Indels 0 Gaps

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Search completed: Job time: 710 sec July1, 2002, 06:28:08

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OM protein - protein search, using sw model .
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Run on:

July 1, 2002, 06:20:23; Search time 25.37 Seconds (without alignments) 32.050 Million cell updates/sec

US-09-461-684-1 109

Title: Perfect score: Sequence:

1 CKKKKKKKKKKKKKKKKKKK 21

BLOSUM62

Scoring table:

Gapop 10.0 , Gapext 0.5

105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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	D 40.0010 - 0.40.1000.	YRO2_YEAST	YD33_YEAST	YG5W_YEAST	KS1_HYDAT	DKC1_HUMAN	NO60_DROME	YNJ1_YEAST	A3D1_HUMAN	YEOI_SCHPO	CBF5_ASPFU	CBF5_EMENI	BRD4_HUMAN

### ALIGNMENTS

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PIR: A48455; A48 PIR: A48455; A48 Phosphorylation; SIGNAL 1 1 CHAIN 186 COMAIN 186 REPEAT 194 REPEAT 202 REPEAT 210 REPEAT 216 REPEAT 226 REPEAT 234 REPEAT 242 REPEAT 250 REPEAT 264 REPEAT 274 REPEAT 274	This SWISS-PROT entry is between the Swiss Institute European Bioinformatiuse by non-profit institute by non-profit instituted and this stateme entities requires a licer or send an email to licer	MEDLINE-93116806; PubMed-147 Deleersnijder W., Prasomsitt Hamers-Casterman C., Hamers "Structure of a Plasmodium c associated with the host ery Mol Biochem Parasitol 56: -i- FUNCTION: DURING INFECTI THE STRUCTURE OF THE RED PARASITE, ALTHOUGH ITS P CYTOPLASMIC FACE OF THE -i- MISCELLANEOUS: ASSOCIATE THROUGHOUT THE ENTIRE ER	LT 1 PLACH PHPA_PLAC 002752; 01-JUL-19 01-JUL-19 01-JUN-19 ACEMA1. PCEMA1. PLASTMODIU EUKATYOLA MCBI_TAXI [1] SEQUENCE
4.4	the Swiss I the Swiss I wean Bioinf on profit and this strequires a n email to	INN-IP-PC1; INN-IP-PC1; INN-IP-PC1; Prasom res-Casterman C., Ham ucture of a Plasmodi ciated with the host Biochem. Parasitol. FUNCTION: DURING INF THE STRUCTURE OF THE PARASITE, ALTHOUGH I SUBCELLULARE OGF MISCELLANEOUS: ASSOC MISCELLANEOUS: ASSOC MISCELLANEOUS: ASSOC MISCELLANEOUS: ASSOC MISCELLANEOUS: ASSOC MISCELLENEOUS: ASSOC	H STANDA  193 (Rel. 26, 194 (Rel. 29, 194 (Rel. 29, 195 (Rel. 29, 195 (Rel. 29, 196 (Rel. 29, 196 (Rel. 29, 197 (Rel. 20, 198 (R
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Antigen; Membrane; Repeat; Erythrocyte. OR 24 (POTENTIAL). ACIDIC PHOSPHOPROTEIN. 16 X 8 AA TANDEM REPEATS. 1-2. 1-3. 1-4. 1-5. 1-6. 1-6. 1-7. 1-8. 1-9. 1-10. 1-11. 1-12. 1-13.	copyright. It is produced through a collaborati- unte of Bioinformatics and the EMBL outstation ics Institute. There are no restrictions on i itutions as long as its content is in no w not is not removed. Usage by and for commerci see agreement (See http://www.isb-sib.ch/announc see(isb-sib.ch).	INN-IP-PC1; INN-IP	D; PRT; 441 AA. Created) Last sequence update) Last annotation update) precursor (50 kDa antigen). Apicomplexa; Haemosporida; Plasmodium.

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Matches 16
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                      InterPro; IPR002687; Nop.
Pfam; PF001798; Nop; 1.
ProDom; PD004104; Nop; 1.
Ribosome biogenesis; Nuclear
DOMAIN 441 511
                                                                                                                                           EMBL; X90565; CAA62165.1; -.
EMBL; Z75217; CAA99630.1; -.
EMBL; AF056070; AAC39484.1; -.
SGD; S0005837; NOP58.
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J. Biol. Chem. 273:16453-16463(1998)
-!- FUNCTION: REQUIRED FOR PRE-18S R
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Pearson B.M., Hernando Y.,
Submitted (AUG-1995) to th
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SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
SIMILARITY: BELONGS TO THE NOP5/NOP56 FAMILY.
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2-1.
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LYS-RICH (BASIC).
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N-LINKED (GLCNAC. . . ) (POTENTIAL).
MW; DB85E83E795EE7E5 CRC64;
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                      protein; rRNA processing ASP/GLU/LYS-RICH.
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InterPro; IPR002478; PUA.
InterPro; IPR002501; TruB_N.
Pfam; PF01472; PUA; 1.
Pfam; PF01509; TruB_N; 1.
SMART; SM00359; PUA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown D., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: BINDS IN UTFRO TO CENTROMERES AND MICROTUBULES. IT CENTROMERE DNA-CBF3-BINDING FACTOR AND IS INVOLVED IN MITOTIC CHROMOSOME SEGREGATION. IT IS ESSENTIAL FOR CELL GROWTH (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           014007:
15-DEC 1998 (Rel. 37, Created)
15-DEC 1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Centromere/microtubule binding protein cbf5 (
5) (Nucleolar protein cbf5).
CBF5 OR SPAC29A4.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
-I- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
-I- SIMILARITY: BELONGS TO THE TRUB FAMILY OF PSEUDOURIDINE SYNTHASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CBF5
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                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                           Microtubules;
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KKEKKEKKEKKEKKKK 472
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                                                   14;
                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                        es; Centromere; Repeat; Nuclear protein; DNA-binding.

7 X 3 AA APPROXIMATE TANDEM REPEATS OF

43 445 1.

450 452 2.

454 456 3.

457 459 4.

460 462 5.

463 465 6.

466 468 7.
                                                   Conservative
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53110 MW;
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70.0%;
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73.7%;
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Pred. No.
                                                               Score 75;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                               B8C9896C5FAEEB71 CRC64;
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SIK1_YEAST

IID SIK1_Y

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Q12460;
01-NOV-1997
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z
Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucabb
Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
Johnston L., Langston Y., Latreille P., Mardis E., Menezes S.,
Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
Taich S., Trevaskis E., Vaudin M., Vignati D., Wilcox L., Wilson
Wohldman P., Waterston R.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribosome biogenesis; No DOMAIN 443 504 MUTAGEN 333 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U20237; AAC49066.1;
EMBL; U14913; AAB67431.1;
SGD; S0004187; SIK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: REQUIRED FOR 60S RIBOSOMAL SUBUNIT
-!- SUBUNIT: INTERACTS WITH NOP1 AND NOP58.
-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gautier T., Berges T., Tollervey D., Hurt E.; "Nucleolar KKE/D repeat proteins Nop56p and Nop58p interact and are required for ribosome biogenesis."; Mol. Cell. Biol. 17:7088-7098(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION, AND MUTAGENESIS. MEDLINE-98038777; PubMed-9372940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S288C / AB972;
Johnston M., Andrews
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae
Cell Growth Differ. 6:789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96040178; PubMed=7547500; Morin P.J., Downs J.A., Snodgrass A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIK1 protein (Nucleolar protein NO SIK1 OR NOP56 OR YLR197W OR L8167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, 01-NOV-1997 (Rel. 35, 16-OCT-2001 (Rel. 40, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE NOP5/NOP56 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002687; Nop.
                                              Similarity
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               Conservative
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                                              68.8%;
70.0%;
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       Pred. No. 0.19
5; Mismatches
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V->A: REDUCED GROWTH RATE AT ALL
TEMPERATURES; WHEN ASSOCIATED WITH R-
Y->C: AT 37 DEGREES, GROWTH SLOWS AFT
TO 8 HOURS AND CELL DIVISION STOPS AF
20 HOURS.
                                                                                                                                                                                        TEMPERATURES; WHEN F8522A5870EF4842
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                                              0.19;
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                                                                                Length 504
                                                                                                                                                                                            ASSOCIATED CRC64;
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Gaps
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                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";

Nature 409:685-690(2001).

-I-FUNCTION: Transcriptional repressor. Binds to the consensus DNA sequence: 5'.GA[GT]AN(GG][AG][CC-3', Might protect cells from apoptosis. Might be involved in pre-mRNA splicing (By similarity).

-I-SUBCELLULAR LOCATION: Nuclear (By similarity).

-I-ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.

-I-TISSUE SPECIFICITY: Widely expressed.
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                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
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01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-116 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wynn S.L., Fisher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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SIMILARITY: CONTAINS 1
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human genomes.";
omics 68:57-62(2000).
                                                                                                                                                                                                                                                                                   regions
                                                                                                                                                                                                                                                                                                      DOMAIN: Contains 8 types of repeats which
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                  AF193606; AAF23120.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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DRBM (DOUBLE-S'
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EMBL; AF193603; AAF23120.1; JC
EMBL; AF193603; AAF23120.1; JC
EMBL; AF193605; AAF23120.1; JC
EMBL; AF193607; AAF23120.1; JC
EMBL; AF193607; AAF23121.1; —
EMBL; AK019312; BAB31536.1; —
EMBL; AK019312; BAB31536.1; —
EMBL; AK0098478; BAB31536.1; —
EMBL; AK0098478; BAB31536.1; —
EMBL; AK008256; BAB25569.1; —
EMBL; AK008256; BAB25569.1; —
EMBL; AK008256; BAB25562.1; —
MGD; MGI:98353; Son.
InterPro: IPR000159; DS_RBD.
InterPro: IPR000147; G_patch, Pfam; PF00035; G-patch; 1.
Pfam; PF00035; G-patch; 1.
PROSITE; PS50174; G_PATCH; 1.
PROSITE; PS50174; G_PATCH; 1.
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AAF23120.1;
AAF23120.1;
AAF23121.1;
BAB31659.1;
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K -> F (IN ISOFORM 2).

MISSING (IN ISOFORM 2).

MW; 648BF28ED3FC01D9 (
                                  Score 75; DB Pred. No. 0.6; 2; Mismatches
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3 X TANDEM REPEATS ([RL]-[RK]-[RF]-S-R.
[G-PATCH.
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14 X 6 AA REF
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                                                                  MEDLINE-99397452; PubMed-10470851; MEDLINE-99397452; PubMed-10470851; Kikuno R., Nagase T., Ishikawa K.-I., Hir Tanaka A., Kotani H., Nomura N., Ohara O. "Prediction of the coding sequences of un The complete sequences of 100 new cDNA cl for large proteins in vitro."; DNA Res. 6:197-205(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SON_HUMAN
P18583; 09
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MEDLINE-21564202; PubMed-11707072;
Reymond A., Friedli M., Neergaard Henrichsen C.,
Deutsch S., Ucla C., Rossier C., Lyle R., Guippon
Antonarakis S.E.;
From PREDs and open reading frames to cDNA Isola
Human Chromosome 21 Transcription Map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (Rel. 16, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2003 (Rel. 41, Last annotation update)
SON protein (SON3) (Negative regulatory element-binding protein) (NRE-binding protein) (DBP-5) (Bax antagonist selected in saccharomyces i)
(BASSI) (Protein C2lorf50).
SON OR NREBP OR DBP5 OR C210KF50 OR KIAA1019.
  MEDLINE=92049296;
                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1999)
                                                                                                                                                                                                                                                                                                                                                         Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen "Human partial CDS from cd34+ stem cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Smooth muscle;
Kawakami T., Noguchi S., Itoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Casadei R., Strippoli P., D'Addabbo P., Canaider S., Vitale L., Giannone S., Carinci P., Zannotti M.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Transcription repression of human hepatitis regulatory element-binding protein/SON."; J. Biol. Chem. 276:24059-24067(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Liver;
MEDLINE=21316479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 78:46-54(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human
Eukaryota; Metazoa;
SEQUENCE OF 554-2426 FROM N.A. (I
MEDLINE=92049296; PubMed=1944255;
                                                                                                                                                                                                                                                              TISSUE=Brain;
                                                                                                                                                                                                                                                                              SEQUENCE OF 437-2426 FROM N.A. (ISOFORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Blood;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "NEDO human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
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5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequencing AUG-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W.-Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11306577;
Y., Wang I.-H., Lo Y.-H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             project.";
EMBL/GenBank/DDBJ
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berdichevskii F.B., Chumakov I.M., Kiselev L. "Decoding of the primary structure of the son genome: identification of a new protein with homology with DNA-binding proteins."; mol. Biol. (Mosk) 22:794-801(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99439804; PubMed-10509013; Greenhalf W., Lee J., Chaudhuri B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Cerebellum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              into mammalian cells."
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"Identification of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 709-1079 FROM N.A. (ISOFORM
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SFRS2/SC-35.
SIMILARITY: CONTAINS 1 G-PATCH DOMAIN.
SIMILARITY: CONTAINS 1 DRBM (DOUBLE-ST
CAUTION: ISOFORM A SEQUENCE FROM REF.7
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InterPro: IPR000467; G_patch.
Pfam; pF00035; dsrm; 1.
Pfam; pF001585; G_patch; 1.
SMART; SM00358; DSRW; 1.
SMART; SM00343; G-patch; 1.
SMART; SM00443; G-patch; 1.
PR0SITE; PS50137; DS_RBD; 1.
PR0SITE; PS50137; DS_RBD; 1.
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AY026895; AAK07692.1; -.
AF435977; AAL30810.1; -.
X63751; CAC6985.1; -.
AB028942; BAA82971.1; -.
X63751; CAA44793.1; ALT_FRAME.
X63731; CAA44793.1; ALT_FRAME.
X63739897; AAD50078.1; -.
X647238; AAB23945.1; -.
X647288; AAB23945.1; -.
X647288; AAB23945.1; -.
X647288; AAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PN0099; PN0099.
182465; -.
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AK024752; BAB14985
AF161428; AAF28988
AF161430; AAF28990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF380182;
AF380183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF380180;
AF380181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF380179; AAL34497.1;
X63753; CAA45282.1; A
M36428; AAA36624.1; -
                                                                                                                                                                                                                                                       Similarity
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1953
1960
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726 895
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                          STANDARD;
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AAL34499.1;
AAL34500.1;
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AAF28990.1;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 1-14.
3 x 11 AA TANDEM REPATS O
P-P-[TME]-[MTG].
4 x 8 AA TANDEM REPEATS O
[AVT]-VT.
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Pred.
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2-1.
2-2.
2-3.
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1-9
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11 X 7 AA TANDEM REPEATS OF
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                        PRT;
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14 X 6 AA REF
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No.
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                        414
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Query Match
Best Local Similarity
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MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus Jannaschii.";
                                                                                                                                                                                                                                                                                                                                                    CBF5_KLULA
013473;
15-JUL-1998
15-JUL-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; MJ0b94;
InterPro; IPRO2687; Nop.
Pfam; PF01798; Nop; 1.
ProDom; PD004104; Nop; 1.
ProDom; PD004104; Nop; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.

349 414 ASP/GLU/LYS-RICH.
DOMAIN 349 414 ASP/GLU/LYS-RICH.
DOMAIN 349 414 ASP/GLU/LYS-RICH.
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01-NOV-1997
16-OCT-2001
                                                                                                                                                                                    Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; Saccharomyc
                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
Centromere/microtubule binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLULA
  Winkler A.A., Bobok A., Hooykaas P.J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 273:1058-1073(1996).
                                                      MEDLINE=98144788; PubMed=9483794;
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U67516; AAB98689.1; TIGR; MJ0694; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanococcus jannaschii.
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                                                                                                                                                             NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377
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                                                                                                                                                                                                                                                                                                   (Nucleolar protein CBF5).
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat)
1 protein MJ0694.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                       Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.98;
                            Zonneveld B.J.M.,
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Pred. No. 0.
2; Mismatche
                                                                                                                                                                                                                                                                                                                       guence update)
notation update)
                                                                                                                                                                                                           Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474
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                                                                                                                                                                                 Kluyveromyces
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0.2;
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                         Steensma H.Y.,
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                                                                                                                                                                                                                                                                                                                          (Centromere-binding factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Best Local
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InterPro; IPR002501; TruB_N
Pfam; PF01472; PUA; 1.
Pfam; PF01509; TruB_N; 1.
SMART; SM00359; PUA; 1.
                                                                                                                                                                                                                                                       CBF5_YEAST
P33322;
01-FEB-1994
01-FEB-1994
15-DEC-1998
                                                            Ol-FEB-1994 (Rel. 28, Created)
Ol-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Centromere/microtubule binding protein CBF5 (Centromere-binding 5) (Nucleolar protein CBF5) (P64').
CBF5 OR YLR175W OR L9470.11.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 SEQUENCE FROM N.A.
STRAIN=S288C / AB9
Johnston M., Andre
                                                         Mol.
                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE=9330283; Pubmed=8336724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The lysine-rich C-terminal repeats of the centromere-binding factor 5 (Cbf5) of Kluyveromyces lactis are not essential for function. ; Yeast 14:37-48(1998).

-I- FUNCTION: BINDS IN VITRO TO CENTROMERES AND MICROTUBULES. IT IS / CENTROMERE DNA-CBR5-BINDING FACTOR AND IS INVOLVED IN MITOTIC CHROMOSOME SEGREGATION. IT IS ESSENTIAL FOR CELL GROWTH. MAY BE: SOME WAY ASSOCIATED WITH THE CBF3 110 kDa SUBUNIT (CBF3A) (BY
                                                                                                                                                                                                                                                                                                                              YEAST
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF008563; AAC64862.1; -.
                                                                                                                                                                                                                                                                                                                                                                                      434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microtubules;
                                                                                                                                                                                                                                                                                                                                                                                                  CENTROMERE DNA-CBF3-BINDING FACTOR AND IS INVOLVED IN MITOTIC CHROMOSOME SEGREGATION. IT IS ESSENTIAL FOR CELL GROWTH. MAY BE IN SOME WAY ASSOCIATED WITH THE CBF3 110 kDa SUBUNIT (CBF3A) (BY SIMILARITY).
SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
SIMILARITY: BELONGS TO THE TRUB FAMILY OF PSEUDOURIDINE SYNTHASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 70.(
14; Conservative
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4443
4449
4552
 / AB972;
Andrews
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                                                                                                                                                                                                                                                                                                               STANDARD;
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  s.
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70.08;
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  Brinkman
                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Nuclear protein; DNA-binding 9 X 3 AA TANDEM REPEATS OF K-K-[D]
                                                                               CBF5p,
                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74; DB 1
Pred. No. 0.22;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95306ECE7FEA756C CRC64;
 R.,
                                                                                  Fouquet C., Car
binds in vitro
                                                                                                                                                                                                                                                                                                               483
 Cooper
                                                                                                                                                                                                                                                                                                               ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Centromere-binding factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 474;
                                                                                              Carbon
Ding
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 Η.,
                                                                                  centromeres
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Best Local :
                                                                                                                                 BRD3_HUMAN STANDARD; PKT; /20 An Q15059; Q92645; 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
Rifken L., Kiles L., Taich A., Trevaskis E., Vignati D.,
Rifken L., Wohldman P., Vaudin M., Wilson R., Waterston R.,
Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.,
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: BINDS IN VITRO TO CENTROMERES AND MICROTUBULES. IT IS A
CENTROMERE DNA-CBF3-BINDING FACTOR AND IS INVOLVED IN MITOTIC
CHOMOSOME SDGREGATION. IT IS ESSENTIAL FOR CELL GROWTH. MAY BE IN
SOME WAY ASSOCIATED WITH THE CBF3 110 kDa SUBUNIT (CBF3A).
-i- SUBCELLULAR LOCATION: NUCLEAR: NUCLEOLAR.
-i- SUBCELLULAR LOCATION: NUCLEAR: NUCLEOLAR.
              TISSUE-Bone marrow;
MEDLINE-96051398; p
                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                Bromodomain-containing
                                                                                                                                                                                                               HUMAN
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD; S0004165; CBF5.
InterPro; IPR002478; PUA.
InterPro; IPR002501; TruB_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                  NCBI_TaxID-9606
                                                                                                          HOMO
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microtubules;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
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                                                                                                                                                                                                                                                                 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                        sapiens (Human)
                                                                                                                   OR RING3L OR KIAA0043.
                                                                                                                                                                                                                                                                             ; L12351; AAA34473.1;
; U17246; AAB67463.1;
S41853; S41853.
                                                                                                                                                                                                                                                               KKEKKEKKDKKEKKEKKEKK 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF01472; PUA; 1.
PF01509; TruB_N; 1.
; SM00359; PUA; 1.
                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                 67.9%; ilarity 70.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       4440
4440
4446
452
458
                                        N.A.
              PubMed=7584044;
                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                 54704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rmatics Institute. There are no resinstitutions as long as its content
 Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat;
                                                                                                                                                                                                                                                                                                                                                                                 WW.
                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                               Score 74; DB
Pred. No. 0.23
5; Mismatches
                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                               10
                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 z
                                                                                                                           otation update)
3 (RING3-like protein).
                                                                                                                                                                                                                                                                                                                                                                                D356B39FDCC32E2D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein; DNA-binding.
3 AA TANDEM REPEATS OF K-K-{DE}.
Sazuka
                                                                                                                                                                                                                                                                                                                            DB 1
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·7
                                                                                                                                                                                                                                                                                                                                        ::
Tanaka
                                                                                                                                                                                                                                                                                                                                        Length 483;
                                                                                                                                                                                                                                                                                                                                                                              CRC64;
Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
Sato
                                                                                                                                                                                                                                                                                                             0;
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CCCCCCL A WAR A WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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MEDLINE-98038990; PubMed-9973153;
Thorpe K.L., Gorman P., Thomas C., Sheer D., Trow
"Chromosomal localization, gene structure and tra
the ORFX gene, a homologue of the MHC-linked RING
Gene 200:177-183(1997).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- TISSUE SPECIFICITY: UBIQUITOUS.
-!- SIMILARITY: CONTAINS 2 BROMODOMAINS.
                 SEQUENCE FROM N.A.

Jiang W., Clifford J., Koltin Y.;

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: BINDS IN VITRO TO CENTROMERES AND MICROTUBULES. IT I

CENTROMERE DNA-CBF3-BINDING FACTOR AND IS INVOLVED IN MITOTIC
CHROMOSOME SEGREGATION. IT IS ESSENTIAL FOR CELL GROWTH, MAY E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             CBF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Centromere/microtubule binding protein CBF5 (
                                                                                                                                                                                                                                                                                                                          Candida albicans (Yeast).
Eukaryota; Fungi; Ascomyc
                                                                                                                                                                                                                                                                      NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                     Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              043101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CBF5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00633; BROMODOMAIN_1; 2. PROSITE; PS50014; BROMODOMAIN_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001487; Bromod
Pfam; PF00439; bromodomain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. entities requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seki N., Kawarabayashi Y., Ishikawa K.-I., Tabata S.; "Prediction of the coding sequences of unidentified human The coding sequences of 40 new genes (KIAAO041-KIAAO080) analysis of cDNA clones from human cell line KG-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bromodomain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 601541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                        (Nucleolar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D26362; BAA05393.1;
281330; CAB03630.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00297;
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   WAY ASSOCIATED WITH THE CBF3 110
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56
11
326
37
487
5676
465
726 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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                                                                                                                                                                                                                                                                                                                                 Ascomycota;
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115
BROMODOMAIN 1.
398
BROMODOMAIN 2.
555
LYS-RICH.
725
SER-RICH.
725
SER-RICH.
466
EL -> DV (IN REF. 2).
79541 MW; 64F526FC3C1033AA CRC64;
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398
555
725
766
466
79541 MW;
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70
                                                                                                                                                                                                                                                                                                                                                                                                                                        CBF5).
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                                                                                                                                                                                                                                                                                              Saccharomycotina;
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Centromere-binding factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
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SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 726
                                                                                                                                                                                                                                                                                                                             Saccharomycetes;
                                                                                                                                                                                                                                                                                                  Candida
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(CBF3A)
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Best Local
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01-JAN-1990
15-JUL-1999
             DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                      Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-89040048; PubMed-2903445;
Trigila T. Stahl H.-D., Crewther
Kemp D.J.;
                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=5837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLAFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01472; PUA; 1.
Pfam; PF01509; TruB, 1.
SMART; SM00359; PUA; 1.
Microtubules; Centromere;
SEQUENCE 479 AA; 54321
                                                                                                                                                                                                                                                                            acid-rich protein (GARP).";
Mol. Biochem. Parasitol. 31:199-202(1988).
 SEQUENCE
                                                                                            CHAIN
                                                                                                                                  PIR; A54514;
                                                                                                                                             EMBL; J03998; AAA29605.1;
                                                                                                                                                                                                                                                                                                                                                                                                                            GARP
                                                                                                                                                                                                                                                                                                                                                                                                                                         Glutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P13816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GARP_PLAFF
                                                                                                                                                                                                                                                                                                     *Structure of a Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; [PR002478; PUA. InterPro; [PR002501; TruB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U59149; AAB94297.1; -.
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SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
SIMILARITY: BELONGS TO THE TRUB FAMILY OF PSEUDOURIDINE SYNTHASES.
                                                                                                                    Malaria; Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 70. 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         acid-rich
             26
120
372
417
576
605
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(Rel. 13, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                  A54514.
 AA;
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70.0%;
                                                                                                                                                                                                                                                                                                                                                                                               (isolate FC27 Apicomplexa; F
                                                                                                                                                                                                                                                                                                                                Crewther P.E.,
 ž
                                                                                                                    Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat; Nuclear protein; DNA-binding MW; 3BAF5104E12C9EB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        precursor.
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                                  GLUTAMIC ACID-RICH PROTEIN.
15 x 3 AA TANDEM REPEATS OF K-K-x.
9 x APPROXIMATE TANDEM REPEATS.
5 x APPROXIMATE TANDEM REPEATS.
POLY-GLU.
               POLY-GLU
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                       X APPROXIMATE
2A8F85606496EA9E CRC64
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                                                                                                                                                                                                                                                                                                                                                                                            / Papua New Guinea).
Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                    gene that encodes a glutamic
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1.35;
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                       TANDEM REPEATS
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RESULT CNG1_HU ID RESULT CNG1_HU ID RECORD CO.
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Best Local
          CNG1_HUMAN STANDARD; PRT; 686 AA.
P29973; Q16485; Q16279;
O1-APR-1993 (Rel. 25, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
cGMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNG-1)
(Cyclic nucleotide gated channel alpha 1) (Cyclic nucleotide gated channel, photoreceptor) (Cyclic-nucleotide-gated channel)
(Rod photoreceptor cGMP-gated channel alpha subunit).
CNGA1 OR CNCG1.
CNGA1 OR CNCG1.
                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1
Hypothetical protein; RNA-bind
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000504; RRM. Pfam; PF00076; rrm; 1. SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin "Identification of novel human genes evolutionarily Caenorhabditis elegans by comparative proteomics."; Genome Res. 10:703-713(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein CGI-79.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=20272150; PubMed=10810093;
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l4; Conservative
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73.7%;
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70.08;
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Pred. No. 0.35
3; Mismatches
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7B6E882D6B192EBE CRC64;
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Pred. No. 0.46;
4; Mismatches
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(Human).

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This SW1
between
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InterPro; IPR000595; cNNP_binding.
Pfam; PF00027; cNNP_binding; 1.
Pfam; PF00520; ion_trans; 1.
SMART; SM00100; cNMP; 1.
                                                                                                                                              EMBL;
                                                                                                                  MIM;
                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dryja T.P., Finn J.T., Peng Y.-W., McGee T.L., Berson E.L., Yau K "Mutations in the gene encoding the alpha subunit of the rod CGMP-gated channel in autosomal recessive retinitis pigmentosa."; Proc. Natl. Acad. Sci. U.S.A. 92:10177-10181(1995).

-i- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTE COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CAN
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MEDLINE-95175019; PubMed-7532814;
Distler M., Biel M., Flockerzi V., Hofn
"Expression of cyclic nucleotide-gated"
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT ARRP PHE-316, AND VARIANTS GLN-28 MEDLINE=96036047; PubMed=7479749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissues and cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yau K.-W., Nathans J.;
"Human rod photoreceptor cGMP-gated channel: amino acid sequence."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ne structure, and functional expression."; Neurosci. 12:3248-3256(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: ROD CELLS IN THE RETINA.
DISEASE: DEFECTS IN CNGAL ARE A CAUSE OF AUTOSOMAL RECESSIVE
RETINITIS PICMENTOSA (ARRP). A DISEASE THAT LEADS TO DEGENERATION
OF RETINAL PHOTORECEPTOR CELLS.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEX WITH CNG4:
SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: RO
                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EWHL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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SUBUNIT: HOMOTETRAMER OR HIGHER OLIGOMER.
                                                                                                                             ; S42457; AAB22778.1;
; S76062; AAD14206.1;
A42161; A42161.
                                                                                                                                                                                                                                                                                                                                  WWW-"http://www.retina-international.com/sci-news/cngalmut.htm"
                                                                                                                                                                                                                                                                                                                                                                    DATABASE: NAME-Mutations of the CNGAl
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PS00888; CNMP_BINDING_1; PS00889; CNMP_BINDING_2;
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Primates;
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Q13428; Q99408;
01-NOV-1997 (Rel
MEDLINE-97250498; PubMed-9096354; Wise C.A., Chiang L.C., Paznekas W.A., Sharma M., Musy M.M., Ashley J.A., Lovett M., Jabs E.W.; "TCOF1 gene encodes a putative nucleolar phosphoprotein that exhibits mutations in Treacher Collins syndrome throughout its coding
                                                                                     MEDLINE-96154183; PubMed-8563749; Dixon J., Edwards S.J., Gladwin A.J., Dixon M.J., Loftus S.K. Bonner C.A., Koprivnikar K., Wasmuth J.J.; "Positional cloning of a gene involved in the pathogenesis of Treacher Collins Syndrome. The Treacher Collins Syndrome
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                                                                                 Collaborative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1997 (Rel. 35, Last sequence update)
2001 (Rel. 40, Last anotation update)
protein (Treacher collins syndrome pr
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L -> I (IN REF. 1).
EE -> HH (IN REF. 1).
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R -> Q.
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GA -> WS (IN REF. 1)
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E5200D216FC97AF6 CRC64;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
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-i- DISEASE: DEFECTS IN TCOF1 ARE THE CAUSE OF TREACHER COLLINS SYNDROME (TCS). TCS IS A AUTOSOMAL DOMINANT DISORDER OF CRANIOFACIAL DEVELOPMENT THAT OCCURS WITH AN INCIDENCE OF 1/50,000 LIVE BIRTHS. THE CLINICAL FEATURES OF TCS ARE BILATERALLY SYMMETRICAL AND INCLUDE: (1) ABNORMALITIES OF THE EXTERNAL EARS, ATRESIA OF THE EXTERNAL EAR CANALS, AND MALFORMATION OF THE MIDDLE EAR OSSICLES, WHICH MAY RESULT IN CONDUCTIVE HEARING LOSS; (2) LATERAL DOMINARD SLOPING OF PALPEBRAL FISSURES, FREQUENTLY WITH COLOBOMAS OF THE LOWER EYELIDS; (3) HYPOPLASIA OF THE MANDIBLE AND ZYGOMATIC COMPLEX; (4) CLEFT PALATE.
                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its content is in no way made the content in the content is in the content in the content in the content is in the content in the content in the content is in the content 
                                                                                  VARIANT
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                                                                                                                                                                                                                                                                                                                                                                             PRINTS;
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Proc. Natl. Acad. Sci. U.S.A. 94:3110-3115(1997).
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U76366; AAC51185.1;

U84664; AAC51185.1;

U84640; AAC51185.1;

U84641; AAC51185.1;

U84642; AAC51185.1;

U84643; AAC51185.1;

U84644; AAC51185.1;

U84645; AAC51185.1;

U84645; AAC51185.1;
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144312 MW; 3880203D985C2699 CRC64;
                                              64.78;
54.88;
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                                             Score 70.5; D
Pred. No. 1.1;
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D -> G.
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Search completed: July 1, 2002, 06:31:33 Job time: 670 sec

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       09h5v6 homo sapien
064075 rattus sp.
09lgx9 arabidopsis
09nt34 homo sapien
09lxr2 arabidopsis
0951v6 macaca fasc
09h6q7 homo sapien
09h648 homo sapien
09h5y3 homo sapien
09h5y3 homo sapien
09er82 mus musculu
09lf6 arabidopsis
077336 plasmodium
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O35807 rattus norv
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 15.2 KDA PROTEIN.
B24H17.160.
        035807
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Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL356815; CAB92638.2; -.
Hypothetical protein.
SEQUENCE 128 AA; 15157 MW; 8C7C65C3DFB70765 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
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Q9H5V6;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA: FLJ22976, F15, CLONE KAT11222 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                             "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AKO26629; BAB15513.1; -
NON_TER 168 168
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Suzuki Y., Obayashi M., Nishi T., Shibahara T., T.
Nakamura Y., Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98172708; pubMed-9511718;
Proels F., Loser B., Marx M.;
"Differential expression of osteopontin, species, during in vitro angiogenesis.";
Exp. Cell Res. 239:1-10(1998).
EMBL; Y08769; CAA70022.1;
EMBL; Y08769; CAA70022.1;
InterPro; IPR000719; Euk_pkinase.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 035807;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MICROVASCULAR ENDOTHELIAL DIFFERENTIATION PROTEIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watanabe K.,
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                                                                                                                                                                 140 KKKKKKKKKKKKKKKKKKK 159
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PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                            20; Conservative (
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Similarity 100.0%;
20; Conservative (
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(TrEMBLrel. 01,
                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                      19549 MW;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                   A19DBD195F8A1A90 CRC64;
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                                                                                                                                                                                                                                                                                                       Length 168;
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Tanaka T.,
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; Murinae; Rat
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O9LGZ9;
O1-CCT-2000 (TrEMBLrel. 15, Created)
O1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, BAC CLONE:F1D9.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Treptophyta; Embryophyta; Treptophyta; Embryophyta; Treptophyta; Brassicales; Brassicaceae; Arabidopsis.
                           Q9NT34 PRELIMINARY; PR
Q9NT34;
Q9NT34;
O1-OCT-2000 (TrEMBLrel. 15, Cret
O1-OCT-2000 (TrEMBLrel. 15, Last
O1-OCT-2000 (TrEMBLrel. 15, Last
HYPOTHETICAL 42.7 KDA PROTEIN ()
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Homo sapiens
                         DKFZP434I1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structural Analysis of Arabidopsis thaliana (Submilted (JUN-2000) to the EMBL/GenBank/DDBJ EMBL; AP002460; BAA97098.1; -. InterPro; IPR001386; Linker_histone. PRINTS; PR00624; HISTONEH5.
SEQUENCE 260 AA; 33307 MW; 43E2394CB813114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamura Y.;
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EMBL; S75997; AAB33384.1; -.
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Mammalia; Eutheria;
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01-DEC-2001 (TrEMBLrel.
NUCLEOPORIN P62 HOMOLOG
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  (Human)
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Rodentia;
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100.0%;
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19, Last annotation update)
PROTEIN (FRAGMENT).
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Pred. No.
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Pred. No.
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Sciurognathi;
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0.00014;
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edons; core eudicots; Rosidae;
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thi; Muridae;
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; Murinae; Rat
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                Q95LV6 PRELIMINARY; PRT; 531 AA.
Q95LV6;
Q05LV6;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 61.4 KDA PROTEIN (FRAGMENT)
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
D'Angelo M., Vezzi A., Modesto D.,
Prangelo M., Vezzi A., Mayer K.F.X.,
Rudd S., Lemcke K., Mayer K.F.X.,
Rudd S., '^^¤°-2000) to the EMBL/(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00646; F-box; 1.
SMART; SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9LXR2;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
HYPOTHETICAL 59.7 KDA PROTEIN.
T20N10_250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AL137556; CAB70810.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 517 AA; 59689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/G
EMBL; AL355032; CAB88307.1; -.
InterPro: IPRO01810; F-box.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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      fascicularis (Crab eating
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                                                                                                                                                                                                                                                                                            h 91.7%;
Similarity 100.0%;
20; Conservative
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42689 MW;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                              MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sto D., Pigazzi M., F.X., Quetier F., EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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  macaque) (Cynomolgus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517
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es 0;
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                                                                                                                                                                                                                                                                                                                                    DB 10;
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Salanoubat
J databases.
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                                                                                                                                                                                                                                                                                                                                Length 517;
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    monkey).
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Best Local :
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Terao K., Sugano S.;
"Isolation of novel full-length cD
libraries.";
Submitted (SEP-2001) to the EMBL/G
EMBL; AB071085; BAB64479.1;
                                                                                       Q9HC48 PRELIMINARY;
Q9HC48;
Q1-MAR-2001 (TrEMBLrel. 16
Q1-MAR-2001 (TrEMBLrel. 16
Q1-DEC-2001 (TrEMBLrel. 19
CTCL TUMOR ANTIGEN SE2-5 (
                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ
EMBL; AKO25632; BAB15196.1; -.
NON_TER 720 720
SEQUENCE 720 AA; 84029 MW; A86586FEAA953D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Kawabata A., Hikiji T., Kobatake N., Inagaki H., Inagaki H., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi Tanaka T., Nakamura Y., Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA: the total Human).
Homo sapiens (Human).
Mefazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
CDNA: FLJ21979 FIS, CLONE HEP06065 (FRAGMENT).
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Mammalia; Eutheria;
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NON_TER 531 53
SEQUENCE 531 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecinae; Macaca.
NCBI_TaxID=9541;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                              692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502
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100.0%;
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                                                                                                                 16, Created)
16, Last sequence up
19, Last annotation
                                                                                            (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 100;
Pred. No.
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Pred. No.
                    Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Catarrhini;
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Catarrhini; Cercopithecidae;
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0.00031;
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ز.
                                             Vertebrata;
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                      Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64
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                                             Euteleostom1;
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Matches 18
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Best Local S
Matches 19
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R Pfam; PF00595; PDZ; 2.

R SMART; SM00228; PDZ; 2.

PROSITE; PS50106; PDZ; 2.

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SECOTORION
O96148; PRELIMINARY; PRT; 483 AA.
O96148; O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-MAY-1999 (TrEMBLrel. 10, Last annotation updat.
HYPOTHETICAL 57.8 KDA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases EMBL; AKO26442; BAB15484.1; .

NON_TER 257 257
SEQUENCE 257 AA; 28778 MW; 100DEA6ABA521868 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-ILEAL MUCOSA:
Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., M
Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., M
Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwar
Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota
Yamada K., Fujii T., Ozaki K., Hirao M., Ohmori Y., Ota
Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura
Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updatcon cona: FLJ22789 FIS, CLONE KAIA2171 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
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EMBL; AF177228; AAG33676.1; -.
HSSP; Q12923; 3PDZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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TISSUE-TESTIS;
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19; Conservative
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667 AA;
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Primates;
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73499 MW;
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Pred. No. 0.0
0; Mismatches
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Pred. No. 0.00063;
1; Mismatches 0
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0.0019;
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i A., Fujiwara T., Ono T
oori Y., Ota T., Suzuki Y
T., Nakamura Y.,
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Best Local :
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                                                                                                                                                                                                                                                                                 "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ
EMBL; AK000295; BAA91063.1; -.
HSSP; Q00420; lAWC.
InterPro; IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ20288 FIS, CLONE HEP04414 (FRAGMENT).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE-99021743; PubMed-9804551;
Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J., Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith Praser C.M., Adams M.D., Venter J.C., Hoffman S.L.;

"Chromosome 2 sequence of the human malaria parasite Plasmodium falcingma".
                                                                                                                                                                                                ANK repeat; Repeat.
NON_TER 686
SEQUENCE 686 AA;
                                                                                                                                                                                                                                  Pfam; PF00023; ank; 14.
SMART; SM00248; ANK; 14.
PROSITE; PS50088; ANK_REPEAT; 13.
PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                             Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Ma
Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Ob
Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T.,
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Mammalia; Eutheria;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 483 AA; 57785 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        falciparum.";
Science 282:1126-1132(1998)
EMBL; AE001382; AAC71836.1;
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                                                                                   666 KRKEKRKKKKKKKKKKKKK
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17; Conserv
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17; Conservative
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73615
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                                                                                                                                             82.6%;
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85.0%;
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3; Mismatches
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0.0037;
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Obayashi M.
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Q9ER82; 01-MAR-2001 Q9ER82

(TrEMBLrel.

16,

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PRELIMINARY;

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Matches 17
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Best Local S
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                                                                                                                    Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kimn S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Myuyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AC007887; AAF79154.1; -
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PRELIMINAKY;
Q9LOF6;
Q9LOF6;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-C57BL/10; TISSUE-SKELETAL MUSCLE;
Kemp T.J., Sadusky T.J., Carey N., Coulton G.R.;
"Murine genes identified from skeletal muscle mRNA which had 7 days of passive stretch in vivo.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ250693; CACOB505.1; -.
NON_TER 1
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                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10090;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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            l Similarity
17; Conserv
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                                                               Score 87; DB 10; Length 107; Pred. No. 0.0022;
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Pred. No. 0.0011;
3; Mismatches 0
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                                                   Mismatches
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annotation update)
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Search completed: July 1, 2002, 06:30:54 Job time: 686 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                              is derived
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length: 2000000000
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                                                                                                                                                                                                                                               Query
Match
                                                                                                                                                                                                                                                                                                                                            is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                               110:
111:
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120:
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                                                                                                                                                                                                                                                                                                                                                                                                                SIDSI/gcgdata/geneseq/geneseqp-embl/AA198.DAT:

SIDSI/gcgdata/geneseq/geneseqp-embl/AA198.DAT:

SIDSI/gcgdata/geneseq/geneseqp-embl/AA198.DAT:

SIDSI/gcgdata/geneseq/geneseqp-embl/AA198.DAT:

SIDSI/gcgdata/geneseq/geneseqp-embl/AA198.DAT:

SIDSI/gcgdata/geneseq/geneseqp-embl/AA198.DAT:

SIDSI/gcgdata/geneseq/geneseqp-embl/AA199.DAT:

SIDSI/gcgdata/geneseq/geneseqp-embl/AA199.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-461-684-1
109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  747574 segs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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                                                                                                                                                                                                                                                 Length
            21
58
70
81
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83
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                                                                                                                           AAO11210
AAO03766
                                                                                                                                                                 AAB13780
AAW45801
AAU18238
                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
Human polypeptide
Human polypeptide
Human polypeptide
Human polypeptide
Novel human DNA-bi
Human colon cancer
Human colon cancer
                                                                                                                                                                                                                                           Description
                                                                                                                                                            One chain of a bom
Novel human DNA-bi
                                                                                                                                                                                                  Soluble peptide an
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âη	AAB59105	21	27	91.7	100	5
ry peptide	888	18	27	91.7	100	4
ery peptide	AAW38801	18	27	91.7	100	₩
	AAW38838	18	27	91.7	100	.5
polypeptid	AA009001	22	26	91.7	100	Ξ
polypeptid	AA008995	22	26		100	0
Human pol	AAO04756	22	26	91.7	100	9
livery peptide	AAW38800	18	26	1	100	8
y peptide	AAW38837	18	26	۳.	100	37
peptide	AAW38880	18	26	۳.	100	6
<	AAW38799	18	25	٠.	100	ິນ
peptide	AAW38836	18	25	1.	100	4
livery peptide	AAW38879	18	25		100	ũ
Delivery peptide u	AAW38798	18	24	91.7	100	ະ
very	AAW38835	18	24	91.7	100	=
	AAW38878	18	24	91.7	100	õ
olypepti	AAO05384	22	23	91.7	100	9
livery	AAW38797	18	23	91.7	100	86
livery peptide	AAW38834	18	23	91.7	100	27
livery peptide	AAW38877	18	23	1.	100	6
y peptide	AAW38796	18	22	1.	100	ŝ
y per	AAW38833	18	22	1	100	4
Sequence of lysine	AAP20159	ω	20	1.	100	ũ
5	AA007806	22	99	2	101	ະວ
	AAU18259	22	54		101	2
polypep	AA000092	22	113	·	102	õ
n immune/hae	AAM90618	22	108	ω.	102	9
human DNA-b	AAU18184	22	108	w	102	8
n colon cance	AAG74650	22	69	ω	102	7
_	AAB42889	21	62	w •	102	6
polypeptid	AA012187	22	60	u	102	ິເກ
polypeptid	AA012203	22	41	ω	102	4
polypepti	AA000291	22	124	94.5	103	ū
Human polypeptide	AA011214	22	68		0	ົວ

## ALIGNMENTS

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RESULT
AAB13780
pk peptide; cytostatic; vaccine; cytotoxic T cell; CTL; immunotherapy;
major histocompatibility complex class 1; MHC class 1; antigen; tumour;
prostate; breast; multiple myeloma.
                                                    Laus
                                     WPI; 2000-442365/38.
                                                                                                                                                Unidentified.
                                                                                                                                                                                                                             AAB13780;
                                                                                                                                                                                                                                           AAB13780 standard; peptide; 21
                                                                   (DEND-) DENDREON CORP.
                                                                                  14-DEC-1998;
                                                                                                  14-DEC-1999;
                                                                                                                22-JUN-2000
                                                                                                                                WO200035949-A1
                                                                                                                                                                                             Soluble peptide antigen pK
                                                                                                                                                                                                             10-NOV-2000
                                                   Hakim I,
                                                                                                                                                                                                             (first entry)
                                                                                  98US-0112324
                                                                                                  99WO-US29724.
                                                   Vidovic
                                                   Ö
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AAO12447 AAU18239

AA011849

AAB53800 AAG73729

Antigens modified by the covalent addition of a peptide that facilitates entry into antigen presenting cells, useful for producing compositions for immunizing against tumors and pathogens -  $\frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}$ 

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RESULT
ADW 45801
ID WAF5801
ADW 45801
ADW 525--
XXX Alpl
AW 67-p
CC CC Wilt
ADW 5801
ADW 67-p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
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This sequence represents one of two identical chains disulphide bonded to form a bombesin dimer. The invention relates to bivalent agonists, with affinity for at least 1 G-protein coupled receptor (GPCR). The
                                                                                                                      Claim 41;
                                                                                                                                                                    Bivalent agonist of G-protein coupled receptors containing two ligand domains - bonded to molecular backbone, for treatment on hypotension, promotion of skin tanning etc., also for delivering and gene therapy vectors to selected cells
                                                                                                                                                                                                                                                                                                                                                                    Carrithers MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                 WPI; 1998-120757/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-melanocyte stimulating hormone; alpha-MSH; receptor agonist; alpha-MSH-ANT; bombesin; dimer; bivalent agonist; disulphide bond;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     One chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW45801 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9803632-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW45801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          μ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 26;
                                                                                                                   Page 48; 71pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of a bombesin dimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Lerner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0686934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US12911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                       MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "This residue is disulphide bonded to the corresponding Cys residue of an identical chain to form a dimer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Epsilon-aminohexanoic acid"
                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                r treatment of for delivering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT
AAU18238
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                         04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on alpha melanocyte-stimulating hormone, MSH). The bivalent agonists are administered orally, by injection or topically. Typical doses for skin tanning are 1-4000 (especially 30-100) mu mole/kg systemically or the bivalent agonists are administered topically in a composition containing 0.001-10 (especially 1) mM. Where both LD are agonists, the bivalent agonist has a synergistically higher activity than two individual agonist ligands, and where at least 1 is an antagonist the effect is stimulatory. The bivalent agonists are active at lower concentrations than known agonists so should avoid toxicity problems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bivalent agonists comprise: (a) two ligand domains (LD), individually agonists or antagonists for GPCR, spaced 40-250 Angstrom apart, and (b) a molecular backbone (MB) covalently bound to LD. The bivalent agonists are useful in human or veterinary medicine as carriers for drugs or gene
                                        07-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy vectors, allowing these to be endocytosed by GPCR-expressing cells. They can also be used e.g. to treat hypertension (angiotensin-based LD); to increase levels of luteinising hormone (LH), using LD derived from LH-releasing hormone, or to promote skin tanning (LD based
                                                                        07-JUL-2000;
                                                                                   28-JUN-2000;
30-JUN-2000;
                                                                                                                 07-JUN-2000;
                                                                                                                                                             16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                 DNA organisation; gene transcription; malignant disease; autoimmune disorder; rheumatic disease; genetic abnormality; infectious disease; neurological disorder; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; DNA-binding protein; histone; chromo domain protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU18238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU18238 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                  18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                     31-JAN-2000;
                                                                                                                                                                                                                                                                     17-JAN-2001; 2001WO-US01305
                                                                                                                                                                                                                                                                                                                            WO200155162-A1
                                                                                                                                                                                                                                                                                                                                                                                        cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromatin organisation modifier; Y-box binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human DNA-binding protein #85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-NOV-2001
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 AA;
         2000US-0214886
2000US-0215435
2000US-0215647
2000US-0216680
2000US-0217487
2000US-0217487
2000US-0217490
                                                                                                               ; 2000US-0198123.
; 2000US-0205515.
; 2000US-0209467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                             2000US-0190076.
                                                                                                                                                                              2000US-0189874.
                                                                                                                                                                                           2000US-0186350.
                                                                                                                                                                                                                                       2000US-0179065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                         2000US-0184664
                                                                                                                                                                                                                         2000US-0180628
                                                                                                                                                                                                                                                                                                                                                                                                       anti-HIV; anti rheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 109; DB 19;
Pred. No. 3.6e-06;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000;

26-JUL-2000; 14-AUG-2000;

14-AUG-2000; 14-AUG-2000;

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The present invention relates to the isolation of novel DNA-binding proteins, and cDNA (AAS29030-AAS29157) and genomic sequences encoding for these proteins. DNA-binding proteins such as histones, chromo (chromatin organisation modifier) domain proteins, and Y-box binding proteins may contribute to diseases resulting from aberrant DNA organisation and/or gene transcription. The sequences of the invention are useful in screening assays to identify antagonists and/or agonists that may enhance or block activities mediated by DNA-binding proteins. Blockers of DNA-binding proteins may be useful in treating disorders such as malignant diseases (e.g. cancer), autoimmune disorders (e.g. diabetes medilitus), rheumatic diseases (e.g. rheumatoid arthritis), genetic abnormalities (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological disorders (e.g. Alzheimer's
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                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                      Claim 11;
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N-PSDB; AAS29114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammanomodulatory activity and activiny insulation activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                           21-NOV-2001
                                                                                       AAU18239
                                                                                                                                AAU18239 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 26339; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAI92378
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18-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                 Conservative
                                         (first entry)
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2000US-0577409
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95.28;
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Pred. No. 1.2e-05;
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Novel human DNA-binding protein

#86.

	14-SEP-2000;	14-SEP-2000;	14-SEP-2000;	14-SEP-2000;	12-SEP-2000;	08-SEP-2000;	08-SEP-2000;	08-SEP-2000;	08-SEP-2000;	00-355-2000	08-SEP-2000;	0002-438-60	0000-1111-000	06-855-2000	06-SEP-2000	05-SEP-2000:	05-SEP-2000;	01-SEP-2000;	01-SEP-2000;	01 - 555 - 2000	01-859-3000	01-SEP-2000	30-AUG-2000	23-AUG-2000	22-AUG-2000	22-AUG-2000	22-AUG-2000	18-AUG-2000	14 - AUG - 2000	14-AUG-2000	14 - 2000 - 2000	14 - AUG - 2000	14 - AIIG - 2000	14 - AUG - 2000	14 - AUG - 2000	14 - AUG - 2000	14 - NOG - 2000	14 - AUG - 2000	14 - AUG - 2000	14 - AUG - 2000	PR 14-AUG-2000; 2000US-0224519.	14-AUG-2000	70 - JUL - 2000	2000	0002 200 51	14-701-2000	11-,700,-2000	11 - Jul - 2000	07-JUL-2000	07 - JUL - 2000	30-JUN-2000	28-JUN-2000	07-JUN-2000	19-MAY-2000	18-APR-2000	17-MAR-2000	16-MAR-2000	02-MAR-2000	24 - FEB - 2000	04 - FEB - 2000	31-JAN-2000		** 1/-JAN-2001; 2001WO-0501305.	17 1 201	PD 02-A0G-2001.	) )	PN W0200155162-AI.		OS Homo sapiens.		KW CYTOSTATIC.	immunomodulatory; an	immercado disease, meniorogical disorder, gene cherapy;	infortions dispasse neurological dispassors appet the property of the property	autoimmune disorder: rheumatic disease: genetic	DNA organisation; gene transcription; malignant dise	chromatin organisation modifier; Y-box binding protein:	KW Human; DNA-binding protein; histone; chromo domain protein;	***	
00 050-2000; 200005-025	05-DEG-2000; 2000US-025	OF DEC 2000; 2000US 025	OF THE 2000; 2000US-025	ON THE COOK SOURCE CASE	01-050-2000 200005-0250	01-050-0000 0000 000	17-NOV-2000, 200000 021	17-NOV-2000; 200000 024	17-NOV-2000: 200005-024	17-NOV-2000 2000115-024	17-NOV-2000: 2000115-024	17-NOV-2000: 2000US-024	17-NOV-2000; 2000US-024	17-NOV-2000; 2000US-024	17-NOV-2000; 2000US-024	1/-NOV-2000; 20000S-024	17-NOV 2000; 200003-024	17-100-2000: 20000: 024	17-NOV-2000: 2000US-024	17-NOV-2000; 2000US-024	17-NOV-2000; 2000US-024	1/-NOV-2000; 20000S-024	17 NOV - 2000; 200005-024	17 NOV 2000; 200003 024	17-NOV-2000, 200003 024	17-NOV-2000; 200003 024	17-NOV-2000: 200008-024	08-NOV-2000: 2000US-024	08-NOV-2000; 20000S-024	00-NOV-2000 3000-024	750-310000 - 0000 - 000 00 + 000	08-NOV-2000: 2000US-024	08-NOV-2000; 2000US-024	08-NOV-2000; 2000US-024	00-NOV-20002 200005-024	08-NOV-2000, 200000-024	08-NOV-2000: 2000US-024	08-NOV-2000: 2000US-024	08-NOV-2000; 2000US-024	08-NOV-2000; 2000US-024	08-NOV-2000; 2000US-024	01-NOV-2000; 20000S-024	20-0CT-2000; 20000S-024	20-0CT-2000; 2000US-024	20 001 2000; 200003-024	20-0CT-2000; 200003-024	20-0CT-2000: 200018-024	20-0CT-2000: 2000IIS-024	20-OCT-2000: 2000US-024	20-0CT-2000: 2000US-024	20-OCT-2000; 2000US-024	13-OCT-2000: 2000US-023	13-OCT-2000: 2000US-023	02-OCT-2000: 2000US-023	02-OCT-2000; 2000US-023	02-OCT-2000; 2000US-023	02-OCT-2000; 2000US-023	02-OCT-2000; 2000US-023	29-SEP-2000; 2000US-023	29-SEP-2000; 2000US-023	29-SEP-2000; 2000US-023	29-SEP-2000; 2000US-023	29-SEP-2000; 2000US-023	27-SEP-2000; 2000US-023	PR 27-SEP-2000; 2000US-0235834.	26-SEP-2000; 2000US-023	25-SEP-2000; 2000US-023	25-SEP-2000; 2000US-023	21-SEP-2000; 2000US-023	21 357 2000; 200005 023	21-SEB-2000, 200003 023	14-SEP-2000: 200000 020	14-SEP-2000: 2000US-023	14-SEP-2000: 2000US-023	14-SEP-2000; 2000US-023					

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RESULT
AAB53800
ID AAB5
XX AAB5
XX AB5
XX O9-W
DT 09-W
DE Huma
XX Huma
KW Ider
KW Immu
KW nepl
KW nepl
KW repz
XX repz
XX X Huma
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Best Local :
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
                                                                                                                                     nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder;
                              Homo sapiens
                                                                                                                                                                                                                                                       Human; colon cancer; colon cancer antigen;
                                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                09-MAR-2001
                                                                                    reproductive disorder; infectious disease; car
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB53800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB53800 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins
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                                                                                                                                                                      mmunomodulatory; muscular; gynaecological; gastrointestinal;
ephrotropic; antiinfective; antibacterial; gene therapy; wou
                                                                                                                                                                                                                                  dentification;
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                                                                                                                                                                                                                                                                                                                 colon cancer antigen protein sequence SEQ ID NO:1340.
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2000US-0254097.
2001US-0259678.
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2000US-0251868.
2000US-0251869.
2000US-0251989.
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                                                                                                                                                                                                                                  cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
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95.2%;
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                                                                                                            gastrointestinal disorder; renal disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58
                                                                                                                                                                                                                      cardioactive; neuroprotective; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 105;
Pred. No. 1
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.5e-05;
                                                                                                                                                                                                                                                    diagnosis;
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Best Local
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29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, system disorders, muscular disorders, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54077 represent sequences used in the exemplification of the present
                                                                                                                            Homo
                                        28-SEP-2000;
                                                                      05-APR-2001
                                                                                               WO200122920-A2
                                                                                                                                                     Human; colon cancer; colon cancer antigen;
colorectal carcinoma; chromosome 14.
                                                                                                                                                                                               Human colon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC9/991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-587534/55
N-PSDB; AAC98557.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC97991 to AAC98763 encode the human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 1920-1921; 2104pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000; 2000WO-US05883
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                                                                                                                            sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                              cancer antigen protein SEQ ID NO:4493.
                                        2000WO-US26524
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                                                                                                                                                                                                                        (first entry)
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99US-0163280
              99US-0157137
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95.2%;
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1.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation.
                                                                                        28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                 26-FEB-2001; 2001WO-US04927
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Pred. No. 1.8e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation cancer.
                                                                                                                                      28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                             (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammation.
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DB; AAI91145.
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DB; AAI89189.
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20; Conservative
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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immuni

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the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                           Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
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                                 The invention relates to
                                                                 Claim 20;
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                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
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18-MAY-2000;
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                    s to human polynucleotides (AAI79941-AAI93841) and (AAO00010-AAO13910) that exhibit activity elating
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95.2%;
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Pred. No. 2.6e-05;
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      The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or activity inhibin activity and may be useful in the diagnosis and/or activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                          Claim 20; SEQ ID NO 26095; 1399pp + Sequence Listing; English
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18-MAY-2000;
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specification, but was obtained in electronic format directly from WIPO
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treatment of cancer,

leukaemia,

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Best Local Similarity
Matches 20; Conser
                                                                                                                                                                             The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopolesis regulating activity, tissue growth factor activity, hammatopolesis regulating activity, tissue growth factor activity. The diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-514838/56
N-PSDB; AAI92118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 26079; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders
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18-MAY-2000; 2000US-0577409
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Matches 20
26
               1 CKKKKKKKKKKKKKKKKKKK 21
l Similarity 95.2
20; Conservative
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46
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                                       Score 102; DB 22;
Pred. No. 3.1e-05;
                                Mismatches
                                              Length 60;
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Search completed: July 1, 2002, 06:19:22 Job time: 509 sec

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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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homeotic protein B
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probable YME1 ATP-
probable Poly-A Bi
hypothetical prote
eyelid - fruit fly
homeotic protein B
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RESULT 2 B87702 ribosomal protein S C; Species: Caulobac C; Date: 20-Apr-2001 C; Accession: B87702 R; Nierman, W.C.; Fe B; Laub, M.T.; De! B; Laub, M.T.; De! n, J; Ermolaeva, M Proc. Natl. Acad. S, A; Title: Complete G, A; Reference number: A; Accession: B87702 A; Status: prelimina: A; Molecule type: DN; A; Cross : references: C; Genetics: A; Gene: CC3652	ب تون	RESULT 1  \$19113  cgcr-4 protein - Chlamydomonas reinhardti C;Species: Chlamydomonas reinhardti C;Species: Chlamydomonas reinhardti C;Species: Chlamydomonas reinhardti C;Date: 13-Jan-1995 #sequence_revision 1: C;Accession: \$1913; \$14466  R;Wakarchuk, W.W.; Mueller, F.W.; Beck, C Plant Mol. Biol. 18, 143-146, 1992 A;Title: Two GC-rich DNA elements of Chla A;Reference number: \$19113; MUID:92119224 A;Accession: \$19113 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-265 <wak> A;Cross references: EMBL:X17208; NID:9181 C;Genetics:</wak>	4444 556 656 663 663 663
protein S16 [imported] : Caulobacter crescentus O Apr-2001 #sequence_rev On: B87702 , W.C.; Feldblyum, T.V.; , W.T.; DeBoy, R.T.; Dodd nolaeva, M.; White, O.; 1. Acad. Sci. U.S.A. 98, Complete Genome Sequence ce number: A87249; MUID:: 01: B87702 preliminary e type: DNA s: 1-165 <sto> eferences: GB:AE005673; I s: 23652</sto>	CI-4  itch 70.6%; al Similarity 82.6%; 19; Conservative AAAAAEAAAAEAAAAAAAAAAAAAAAAAAAAAAAAAA	chlamyd anydonnas allyl13; S14 ./w.; Muell 11, 18, 143 C-rich Dna C-rich Dna 11, 113 11, 113 1	59.6 59.6 58.7 58.7 58.7 58.7 57.8 57.8
6 [imported] - Ca cer crescentus #sequence_revisio dblyum, T.V.; Pau boy, R.T.; Dodson, White, O.; Salz ii U.S.A. 98, 413 nome Sequence of A87249; MUID:2117 Y	70.6%; 82.6%; ative ahaaeaaaa            Vaaearaa	amydomonas r onas reinhar onas reinhar #sequence_re #sequence_re \$14466 Unda-146, 19 DNA element S19113; MUID y y	644 2 703 2 109 1 109 1 109 1 1074 2 1075 2 1075 2 1079 2 179 2 179 2 568 2 568 2 568 2 646 2
- Caulobac ision 20-A Paulsen, son, R.J.; Salzberg, 4136-4144 of Caulob 21173698; VID:g13425	Score 77; Pred. No. 1; Mismatc 25	3-J	2 S39356 2 T48600 2 T48600 1 R6UTP1 1 B148423 2 T13232 2 T13229 2 T13229 2 T13229 2 T13229 2 T13229 2 T13229 3 T146231 4 A46231 4 F2908 4 F2908 3 T34823 3 T34823 4 S52418 2 S52418 ALIGNMENTS
#text_c #text_c =lson, K A.S.; napiro, napiro, 259647	2; Length 2 8; 3; Indel	<pre>itii (fragment) 13-Jan-1995 #text_change , C.F. nlamydomonas reinhardtii . 224 18136; PIDN:CAA35080.1; P</pre>	
20-Apr-200 lisen, J.; M.L.; Hai mter, J.C.	.s 0; Gaps	nge 21-Jul-2000 ii with complex ; PID:gl8137	transcription fact kinase like protei acidic ribosomal phomeotic protein edachshund isoform dachshund protein dachshund protein dachshund protein habdominal segment female sterile hom 50s ribosomal protein sparaginyl-trna sconserved hypothest GTP-binding regula
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Matches 18; Conserv

Conservative

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66.1%; 75.0%;

Score 72; DB 2; Pred. No. 0.62; 2; Mismatches

2; 4.

Length 165; Indels

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Gaps

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engrailed homeodomain-containing protein En-1 - mouse
N:Alternate names: homeotic protein En-1
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C:Accession: A48423; S13009; A26629; A24778
R:Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.;
Dev. Genet. 13, 345-358, 1992
A;Title: Cloning and sequence comparison of the mouse, human, and chicken er
A:Reference number: A48423; MUID:93185339
A;Accession: A48423
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
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cgcr-1 protein
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A:Residues: 1-183 <ROB>
A:Cross-references: EMBL:X67142; NID:g17792; PID:g17793
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C;Species: Brassica napus (rape)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
C;Accession: S24960
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A;Residues: 1-205 <WAK>
A;Cross references: EMBL:X17207
C;Superfamily: phage lambda hypothetical protein 401
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R:Wakarchuk, W.W.; Mueller, F.W.; Beck, C.F.
Plant Mol. Biol. 18, 143-146, 1992
A;Title: Two GC-rich DNA elements of Chlamydomonas reinhardtii with complex arrangements
A:Reference number: S19113; MUID:92119224
A:Accession: S19114
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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F:1-23/Domain: signal sequence *status predicted <SIG>
F:24-48/Domain: propeptide *status predicted <PRO>
F:49-96/Product: antifreeze protein *status predicted <MAT>
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A; Title: Expression during 6
A; Reference number: A24778;
A; Accession: A24778
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A;Title: Structural variations in the alanine-rich antifreeze
A;Reference number: S02376; MUID:88029483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antifreeze protein precursor - yellowtail flounder C;Species: Limanda ferruginea (yellowtail flounder) C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 C;Accession: S02376
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C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;313-369/Domain: homeobox homology <HOX>
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A; Residues: 1-97 <SCO>
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A; Residues: 311-401 <JO2>
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A;Residues: 278-401 <AGOY>
A;Cross-references: GB:Y00201;
R:Joyner, A.L.; Kornberg, T.; (
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Genes Dev. 1, 29-38, 1987
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A; Residues: 321-380 <HOL>
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A;Reperimental source: CD-1, embryo
A;Experimental source: CD-1, embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:126620)
R;Holland, P.W.H.; Williams, N.A.
FEBS Lett. 277, 250-252, 1990
A;Title: Conservation of engrailed-like homeobox sequences during vertebrate
A;Teference number: S13009; MUID:91099509
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                                         2 EAAAAAEAAAAEAAAAAEAAAAA 25
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sex comb protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13748
R;Sinclair, D.A.R; Milne, T.A.; Hodgson, J.W.; Shellard, J.; Salinas, C.A.; in Development 125, 1207-1216, 1998
A;Title: The Additional sex combs gene of Drosophila encodes a chromatin prot.
A;Reference number: Z17750; MUID:98146384
A;Accession: T13748
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Species: Drosophila melanogaster
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C:Accession: S16356
R:Mevel-Ninio, M.; Terracol, R.; Kafatos, F.C.
EMBO J. 10, 2259-2266, 1991
A:Title: The ovo gene of Drosophila encodes a zinc A:Reference number: S16356; MUID:91293102
A:Accession: S16356
A:Status: preliminary
A:Status: preliminary
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A; Title: Multiple products from the shavenbaby-ovo gen. A; Reference number: A56038; MUID:95021209
A; Accession: A56038
A; Status
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A56038
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A;Introns: 931/3; 1152/3
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A; Residues: 1-1213 <MEV>
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A;Molecule type: mRNA
A;Residues: 1-1028 <GAR>
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Pred. No. 5.
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4.6;
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5.2;
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                                                              chromatin protein that
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                                                                                                 Kyba, M.;
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A; Cross-refe
C; Keywords:
                                                                          A; Molecule type: mRNA
A; Residues: 1-655 < CRE>
A; Cross-references: GB:M19020;
                                                                                                                                     R:Crews, S.T.; Thomas, J.B.; Goodman, C.S. Cell 52, 143-151, 198
A:Title: The Drosophila single-minded gene A:Reference number: A29945; MUID:88151023
A:Accession: A29945
                                                                                                                                                                                                                                                    neurogenesis regulatory protein - fruit fly (Drosophila melanogaster) (fragment) N;Alternate names: single-minded gene protein C;Species: Drosophila melanogaster C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: sucB; NMA1150
C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding
C;Keywords: acyltransferase; coenzyme A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references:
C;Function:
A;Description: invol
                                          A; Gene: sim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) E2 component NMA1150
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 *sequence_revision 05-May-2000 *text_change 02-Feb-2001
C;Accession: A81882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-1668
A:Cross-references:
C;Genetics:
                                                                                                                                                                                                                                          C; Accession: A29945
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A;Experimental source: serogroup
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A; Residues: 1-403 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis A; Reference number: A81775; MUID: 20222556 ·
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Best Local S
Matches 18
Cross-references: FlyBase:FBgn0004666
Keywords: DNA binding; transcription
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: EMBL:AJ001164; NID:g3292938; PIDN:CAA04568.1; PID:g3292939
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78.3%;
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                                                                            NID:g158464;
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A, strain Z2491
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62.48; 66.78;

Score 68; DB Pred. No. 4.2;

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Length 655

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polycomb protein enhancer - fruit fly (Drosophila melanogaster) (;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 1 C;Accession: T13154 R;Stankunas, K.; Berger, J.; Ruse, C.; Sinclair, D.A.; Randazzo, Development 125, 4055-4066, 1998 A;Title: The enhancer of polycomb gene of Drosophila encodes a ch A;Reference number: 217611; MUID:98407961 A;Accession: T13154
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C;Genetics:
A;Gene: FlyBase:Dvir/Eip74EF
A;Cross references: FlyBase:Bgn0013076
C;Superfamily: ets DNA-binding domain homology
F;779-859/Domain: ets DNA-binding domain homology
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C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 21-Feb-1997
C:Accession: B53225
R:Jones, C.W.; Dalton, M.W.; Townley, L.H.
Genetics 127, 535-543, 1991
A:Title: Interspecific comparisons of the structure and regulation of the D A; Reference number: A53225; MUID:91200627
A; Accession: B53225
      paire1 type homeobox protein, NBP
C:Species: Homo sapiens (man)
C:Date: 16-Apr-1997 #sequence_revi
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A;Residues: 1-2023 <STRA>
A;Cross-references: EMBL:AF079764; NID:g3757889; PID:g3757890; PIDN:AAC64271.1
A;Experimental source: imaginal disc
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nes 18; Conserv
  es: Homo sapiens (man)
16-Apr-1997 #sequence
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#sequence_revision 09-May-1997 #text_change 24-Sep-1999
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9.5;
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A;Contents: neuroblastma cell
A;Accession: JC5273
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-314 <YOK>
A;Cross-references: DDB:DB2344; NID:q1841337; PIDN:BAA11555.1; PID:cC;Comment: This protein is a transcriptional repressor involved in reC;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;99-155/Domain: homeobox homology <HOX>
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C:Superfamily: Phaseolus glycine-rich cell wall protein
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submitted to the EMBL Data Library, May 1998
A:Description: The sequence of C. elegans co.
A:Reference number: 21284
A:Accession: T33110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C18H7.3 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 29-Oct.1999 #sequence_revision 29-Oct.1999 #t. C;Accession: T33110
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                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-460 <TIN>
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R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
DNA Res. 3, 311-320, 1996
A;Title: Identification and cloning of neuroblastoma-specific and nerve tissue-speci A;Reference number: JC5272; MUID:97191543
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Best Local Similarity 75.8
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30S ribosomal protein S16.
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267 COILED COIL (POTENTIAL).

518 ALA/PRO-RICH.

114 LGSATAKLS -> SASAIQLAA (IN REF. 2).

119 A -> S (IN REF. 2).

183 A -> AMVEADLERAEERA (IN REF. 2).

184 A -> L (IN REF. 2).

195 V -> L (IN REF. 2).

231 NOREEEYKNQIKTLNTR -> TOKEETFETOIKY
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     Score 72; DB 1;
Pred. No. 0.18;
2; Mismatches
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A -> AMVEADLERAEERA (IN REF. 2).
V -> L (IN REF. 2).
NOREEEYKNOLKTLNTR -> TOKEETFETQIKYLDHS
(IN REF. 2).
; 153D0872CF9DB6EA CRC64;
                                                                                                                                ED46FC2798C5BE1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subdivision; Caulobacter group;
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RESULT 4
HME1_MOUSE
ID HME1_MOUSE
AC P09065;
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OLEC_BRANA
ID OLEC_B
AC P29526
DT 01-APR
DT 11-APR
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P29526;
01-APR-1993
01-APR-1993
15-JUL-1998
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DOMAIN
SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
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Roberts M.R., Hodge R., Ross J.H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Anther;
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                                                                                                                                   151
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                                                                                                                                                                                                                                        Similarity
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183 /
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8 (Rel. 36, La
8 (Fragment).
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78.3%;
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MW; 198A5D3B6DF3045A CRC64;
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PIR; A26629; A26629.

PIR; A24778; A24778.

PIR; S13009; S13009.

PIR; A48423; A48423.

HSSP; P02836; 3HDD.

TRANSFAC; T02016;
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01-FEB-1994 (Rel. 2
16-OCT-2001 (Rel. 4
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                                                                        PROSITE;
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                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                    PROSITE; PS00027;
                                                                                                                   SMART; SM00389; HOX;
                                                                                                                              PRINTS; PR00026; ENGRAILED. PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                             Pfam; PF00046;
                                                                                                                                                                        InterPro; IPR000747; Engrailed InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                    TRANSFAC; T02016; -. MGD; MGI:95389; En1.
                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Conservation of engrailed-like homeobox sequences during evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 321-380 FROM N.A. MEDLINE=91099509; PubMed=1980115; Holland P.W.H., Williams N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Logan C., Hanks M.C., Noble-Topham Provart N.J., Joyner A.L.;
"Cloning and sequence comparison of engrailed genes reveal potential fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
                                              DOMAIN
                                                            Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett. 277:250-252(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Expression during embryogenesis of a mouse gene with homology to the Drosophila engrailed gene."; lell 43:29-37(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 298-401 FROM N.A. MEDLINE-86079501; PubMed-2416459; Joyner A.L., Kornberg T., Coleman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila engrailed gene: expression Genes Dev. 1:29-38(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 278-401 FROM N.A. MEDLINE-88112776; Pubmed-2892757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-93185339; PubMed-1363401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homeobox
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"En-1 and En-2, two mouse genes with sequence homology to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regions.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE ENGRAILED FAMILY OF HOMEOBOX PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR EN-1
                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Ex European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content field and this statement is not removed. Usage by and
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                                                                        PS50071;
PS00033;
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52 87.
73 87.
207 228
312 371
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                                                                      HOMEOBOX_1; 1.
HOMEOBOX_2; 1.
ENGRAILED; 1.
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Rodentia;

    Developmental protein; N
    PRO-RICH.
    POLY-PRO.
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    HOMEOBOX.

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DT 01-OCT-1996 (Rel
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                                                                                                                                                                                                                                         SIGNAL
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antifreeze protein precursor (AFP).
Limanda ferruginea (Yellowtail flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Pleuronectidae; Limanda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-88029483; PubMed-3665937; Scott G.K., Davies P.L., Shears M.A., Fletcher G.L.; "Structural variations in the alanine-rich antifreeze pleuronectinae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          EUR: J. Blochem. 168:629-633(1987).
-:- FUNCTION: ANTIFREEZE PROFEINS LOWER THE BLOOD
-:- SIMILARITY: BELONGS TO THE TYPE-I AFP FAMILY.
ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1988
01-AUG-1990
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                                                                                                                                                                                                                                                                Antifreeze
                                                                                                                                                                                                                                                                          InterPro; IPR000104; Antifree PRINTS; PR00308; ANTIFREEZEI.
                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                    HSSP;
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18; Conser
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                                                                                                                                                                                                                                                               protein;
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(Rel. 34, Created)
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(Rel. 09, Last sequence up
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TYPE 1 AFP ARE
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sequence

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16-OCT-2001
Ovo protein
OVO OR SVB.
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PRINTS; PR00048; ZINCFINGER.

SMART; SM00355; ZINC_FINGER_C2H2_1; 3.

PROSITE; PS00028; ZINC_FINGER_C2H2_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95021209; PubMed-7935398; Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; "Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaster: relationship to genetic complexity."; mol. Cell. Biol. 14:6809-6818(1994).
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EMBL; X59772; CAB36921.1;
HSSP; P25490; 1ZNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0003028; ovo
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000822;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91293102; PubMed-1712294;
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OJ. 10:2259-2266(1991).

OJ. 10:259-2266(1991).

OJ. 10:259-2266(1991).

OJ. 10:259-2266(1991).

OJ. 10:259-2266(1991).

OJ. 10:259-2266(1991).

OF FEMALE LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.

SUBCELLULAR LOCATION: Nuclear (Potential).

SUBCELLULAR LOCATION: Nuclear (Potential).

DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DURING OOGENESIS. STORED IN THE EGG BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINUED PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanogaster (Fruit fly)
  (Rel. 40, Last annotat (Shaven baby protein).
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152
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POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-ALA.
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POLY-ALA.
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POLY-GLY.
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POLY-GLY.
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ota; Diptera; Brachycera; Musc
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RESULT

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AC P05709; 096521; Q9VFZ3;
DT 01-WOV-1988 (Rel. 09, Cre.
DT 01-MAY-1992 (Rel. 40, Las
DT 16-OCT-2001 (Rel. 40, Las
DT 16-OCT-2001 (Rel. 40, Las
DT 16-OCT-2010 (Rel. 40, Las
RA MEDLINE-92103681; PubMed-ARA MEDLINE-92103681; PubMed-RA MEDLINE-99054545; P
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Best Local
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Bontova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-18 FROM N.A., AND SIMILARITY TO HLH PROTEINS. MEDLINE-92103681; PubMed-1760843; Nambu J.R., Lewis J.O., Wharton K.A. Jr., Crews S.T.; "The Drosophila single-minded gene encodes a helix-loop-helix protein that acts as a master regulator of CNS midline development."; Cell 67:1157-1167(1991).
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             control of single-minded transcription by dorsal/ventral patterning
genes,";
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Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kasai Y., Stahl S., Crews S.;
"Specification of the Drosophila CNS midline cell lineage: direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88151023; PubMed=3345560; Crews S.T., Thomas J.B., Goodman C.S.;
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hropoda; Tracheata; Hexapoda; Insecta;
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gebbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liu X., Mattei B., Kolitas T.C., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., Wolltosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syles B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Polong W., Zhou S., Zhu X., Smith H.O.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M.
                                                                                                                                                                                                                                                 FlyBase; FBg0004666; sim.
InterPro; IPR003015; HLH_Myc.
InterPro; IPR001092; HLH_dim.
InterPro; IPR0010192; PAC.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS.
Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 2.
SMART; SM00086; PAC; 1.
SMART; SM00088; HELIX_LOOP_HELIX; 1.
PROSITE; PS00138; HELIX_LOOP_HELIX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M19020; AAA28900.1; --
EMBL; AF071934; AAC64519.1; ALT_SEQ
EMBL; AE003698; AAF54902.1; ALT_SEQ
PIR; A29945; A29945.
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SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY TRANSCRIPTION FACTORS.
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European Bioinformatics Institute. There a
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RESULT 8
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D. Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D. Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Borthier P., Bouck J., Butler H., Cadieu E., Center A., Chandra I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95372400; PubMed-7644522; Sutherland J.D., Kozlova T., Tzertzinis G., Kafatos F.C.; "Drosophila hormone receptor 38: a second partner for Dros suggests an unexpected role for nuclear receptors of the reactor-induced protein B type."; Proc. Natl. Acad. Sci. U.S.A. 92:7966-7970(1995).
                                                                                                                                                                                                                                                                        MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                    Kozlova T., Pokholkova G.V., Zhimulev I.F., Kafatos F.C.; "Drosophila hormone receptor adult cutticle formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (SHORT ISOFORM), AND TISSUE SPEC FICITY MEDLINE-98370123; PubMed=9704500; Komonyi O., Mink M., Csiha J., Maroy P.; "Genomic organization of DHR38 gene in Drosophila: presence "Genomic organization of DHR38 gene in Drosophila:
                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY,
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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NCBI_TaxID=7227;
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POLY SER.
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MISSING (IN REF. 4).
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Doubin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.C.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wel M.-H., Ibegwam C.,
RA Linking M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shide B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng R.A., Wyers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation, regulation, and DNA-binding properties of three
and Drosophila nuclear hormone receptor superfamily members.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:10604-10608(1995).
C. -i- FUNCTION: BINDS TO NGFI-B RESPONSE ELEMENTS. PLAYS AN IMPORTANT
C. -I- SUBBUNIT: FORMS A HETERODIXER WITH USP.
C. -i- SUBGELLULAR LOCATION: NUCLEAR
C. -i- SUBGELLULAR LOCATION: NUCLEAR
C. -i- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
C. SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
C. -i- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN PREBLASTODERM
C. -i- TISSUE SPECIFICALLY IN CENTRAL NERVOUS SYSTEM AND INTESTINAL
C. TRACT. HIGHLY EXPRESSED IN THIRD INSTAR LARVAL IMAGINAL DISKS AND
C. BRAIN COMPLEXES, BUT NOT IN OVARIES.
C. HIGHER IN LATE EMBRYOGENESIS AND DURING LARVAL AND PUPAL STAGES.
C. SHORT ISOFORM IS ENRICHED IN PUPAE AND ADULTS, LONG ISOFORM IN
                     FlyBase; FBgn0014859; H
InterPro; IPR000536; Ho
InterPro; IPR001723; St
InterPro; IPR001528; zf
Pfam; PF00104; hormone_
                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                            .; X89246; CAA61534.1; -.
.; Y15606; CAA75690.1; -.
.; AE002073; CAA05172.1; -.
.; AE003667; AAF53914.1; -.
L; U36762; AAC46926.1; -.
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AE003667; AAF53914.1;
U36762; AAC46926.1;
P19793; 2NLL.
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SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
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hormone_rec; 2.
zf-C4; 2.
                                            Strdhormone_receptor zf-C4.
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                                                                   "Paired-like homeodomain proteins Phox2a/Arix and Phox2b/NBPhox have similar genetic organization and independently regulate dopamine beta-hydroxylase gene transcription.";
DNA Cell Biol. 19:539-554(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Createu, 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Paired mesoderm homeobox protein 2B (Paired-like homeobox 2B) ρη το μοιχ2B homeodomain protein) (Neuroblastoma Phox) (NBPhox).
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Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Alternative splicing; Developmental protein.
DNA_BIND 744 809 NUCLEAR RECEPTOR-TYPE.
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                   MEDLINE=99326521; PubMed=10395798,
                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                               PubMed=11034547;
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S -> L (IN REF. 1 AND 3).

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A -> D (IN REF. 2).

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POLY-SER.
POLY-GLN.
POLY-ALA.
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POLY-THR.
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Paired mesoderm homeobox protein 2B (Paired-like homeobox 2B)
MEDLINE-98040559; PubMed-9374403;
Pattyn A., Morin X., Cremer H., Goridis C., Brunet J.-F
"Expression and interactions of the two closely related
genes Phox2a and Phox2b during neurogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
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                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                     (PHOX2B homeodomain protein) (Neuroblastoma Phox) (NBPhox)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             035690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50071; HOMEOBOX_1; 1.

PROSITE; PS50071; HOMEOBOX_2; 1.

Transcription regulation.

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                                                                                                                                                                                                                                                                                                                                                                                             PMX2B OR PHOX2B.
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TRANSCRIPTION FACTOR WHICH COULD DETERMINE A NEUROTRANSMITTER

PHENOTYPE IN VERTEBRATES. ENHANCES SECOND-MESSENGER-MEDIATED

ACTIVATION OF THE DOPAMINE BETA-HYDROYLASE AND C-FOS PROMOTERS,
AND OF SEVERAL ENHANCERS INCLUDING CYCLIC AMP-RESPONSE ELEMENT AND

SERUM-RESPONSE ELEMENT.

SUBCELLULAR LOCATION: NUCLEAR (By similarity).

TISSUE SPECIFICITY: EXPRESSED IN NEUROBLASTOMA, BRAIN AND ADRENAL
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78.3%;
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Pred. No.
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POLY-GLY.
POLY-ALA.
POLY-ALA.; 76737F71948B5D81 CRC64;
                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Sciurognathi; Muridae,
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                                                                                                                                                                                     MAZ_HUMAN STANDARD; PRT; 477 AA. P56270; 099443; Q15703; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Myc-associated zinc finger protein (MAZI) (Purine-binding transcription factor) (Pur-1) (ZF87) (ZIF87).
                                                                                                                                              Eukaryota;
Mammalia; F
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SEQUENCE FROM N.A. TISSUE-Carcinoma;
                                       regulating t
Proc. Natl.
                                                              Bossone S.A., Asselin C., Pa
MAZ, a zinc finger protein,
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                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1100882; Pmx2b.
MGD; MGI:1100882; Pmx2b.
InterPro; IPR000047; HTH_repre
InterPro; IPR001356; Homeobox; 1.
                                                                                         MEDLINE-92366479;
                                                                                                                             NCBI_TaxID=9606;
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PRINTS; PR00031; HTHREPRESSR.
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                                                                                                                                                                     Homo sapiens (Human)
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-1- SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.
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[2]
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                                                                                                                                            ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A., Asselin C., Patel A.J., Marcu K.B.; nc finger protein, binds to c-MYC and C2 gen transcriptional initiation and termination. Acad. Sci. U.S.A. 89:7452-7456(1992).
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                       PubMed=1502157;
                                                                                                                                            Chordata;
Primates;
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78.3%;
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; 40737E71948B595A CRC64;
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AX SONG J., MUTAKAMI H., TSUTSUI H., TANG X., MATSUMURA M., ITAKURA K., KANAZAWA I., Sun K., YOKOYAMA K.K.;

KANAZAWA I., Sun K., YOKOYAMA K.K.;

TGENOMIC OFGANIZATION AND AFFINITY FOR THE FORMER. ANASCRIPTION FACTOR WITH DUAL ROLES IN TRANSCRIPTION INITIATION AND TERMINATION. BINDS TO TWO SITES, MEIAI AND MEIA2, WITHIN THE C-MYC PROMOTER HAVING GREATER AFFINITY FOR THE FORMER. ALSO BINDS TO MULTIPLE G/C-RICH SITES.

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CHITCHE PROMOTER OF THE SPI FAMILY OF TRANSCRIPTION FACTORS.

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                                                                                                                                   InterPro; 1PROVULL, 6.
Pfam; PF00096; zf-C2H2; 6.
PRINTS; PRO0048; ZINCFINGER.
SMART; SM00355; ZNF_C2H2; 6.
SMO355; ZNF_C2H2; 6.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
PROSITE; PS0157; ZINC_FINGER_C2H2_2; 5.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to two sites within the c-myc promoter.";
Biochemistry 31:4102-4110(1992).
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"The serotonin la receptor gene contains responds to MAZ and Spl.";
                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                TRANSFAC; T00490; -. TRANSFAC; T02305; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pancreatic islets; MEDLINE-96428591; PubMed-8831693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92232709; PubMed=1567856; Pyrc J.J., Moberg K.H., Hall D.J.; "Isolation of a novel cDNA encoding
                                                                                                                                                                                                                                                                  MIM; 600999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUSCLE, AND PANCREAS. SEEMS NOT TO BE EXPRESSED IN KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Lymphoblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pancreatic islet cells."
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M9339; -; NOT_ANNOTATED_CDS.
D95131; BAA12728.1; ALT_INIT.
U33819; AAB04121.1; ALT_INIT.
AB017335; BAA33064.1; -.
                                                                                                                                                                                                                                                                                                              P08046;
   ; Repeat;
190 4;
190 3;
190 3;
279 3;
307 3;
366 3;
392 4;
196 10
157 16
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RESULT RESULT REAL PROPERTY OF THE NAME OF
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Best Local
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01-AUG-1991
01-AUG-1991
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                             EMBL; X56682; CAA40011.1; -. PJIR; S13367; S13367. HSSP; P22808; IVND. F1yBase; FBgn0012114; Dana\B. InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _DROAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Retrotransposon-induced overexpression of a defects in eye morphogenesis in Drosophila."; EMBO J. 10.407-417(1991).
-i- FUNCTION: Probably involved in eye morpho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila ananassae (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Trac
Pterygota; Neoptera; Endopterygota;
    SEQUENCE
                                                                                                                                 DNA_BIND
                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                  DNA-binding;
                                                                                                                                                                                                                                        PROSITE; PS00027; PROSITE; PS50071;
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                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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NCBI_TaxID=7217;
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SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEOBOX PROTEINS
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AAAQESAAAAAAAAAAAAAAAAA 111
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(Rel. 19,
(Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Drosophilidae; Drosophila.
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Last sequence update)
                                                     Developmental protein; Nuclear protein; Vision.
HIS/GLN-RICH (OPA-REPEAT).
HIS/GLN-RICH (OPA-REPEAT).
HIS/PRO-RICH.
OPA-REPEAT).
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POLY-ALA.
MISSING (IN REF. 3).
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MISSING (IN REF. 3).
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oda; Tracheata; Hexapoda; Insecta;
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                    ALA-RICH.
PRO-RICH.
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AA7B8B6367370FBB CRC64;
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HXAD_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              DOMAIN
DOMAIN
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HSSP; P02833; 1SAN.
TRANSFAC; T03337; -.
MGD; MGI:96173; HOXA13.
InterPro; IPR001356; Homeobox.
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                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
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Nat.
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Q62424;
                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                    DNA_BIND
                                                                                                                                                                                                                                                                                                                             Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mortlock D.P., Post L.C., Innis J.W.; "The molecular basis of hypodactyly (Hd): a deletion to arrest of digital arch formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                        Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=96259555; PubMed=8673126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID+10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220
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Genet. 13:284-289(1996).

FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF THE PROVIDES CELLS WITH A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (ESTMILARITY).

SUBCELLULAR COCATION: Nuclear:

DISEASE: DEFECTS IN HOXA13 ARE THE CAUSE OF HYPODACTYLY (HD), A CONDITION CHARACTERIZED BY PROOFOUND DEFICIENCY OF DIGITAL ARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURES.
SIMILARITY: BELONGS TO THE ABD-B FAMILY OF HOMEOBOX PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAAEAAAAAEAAAAA 25
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         l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                          SM00389; HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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18; Conservative
                                                                                                                                                                                                                                                                                                                                                 DNA-binding; Developmental protein;
                                                                                                                      386
                                                                                                                                                                  38
320
52
62
73
101
116
       Conservative
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                                                                                                                                            379
57
66
84
104
133
205
                             60.6%;
70.8%;
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78.3%;
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    Score 66; DB
Pred. No. 1.4;
2; Mismatches
    2
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                                                                                                                                                                POLY - ALA.
HOMEOBOX.
POLY - GLY.
POLY - ALA.
POLY - ALA.
POLY - ALA.
POLY - ALA.
                                                                                                                                               POLY-ALA
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                                                Length 386;
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-i FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

-i SUBCELLULAR LOCATION: Nuclear.
-i SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                       InterPro; IPR001356; Homeobox. Pfam; PF00046; homeobox; 1. SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HXAD_HUMAN STANDARD; PRT; 388 AA. P31271; 043371; 01-JUL-1993 (Rel. 26, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Homeobox protein Hox-A13 (Hox-1J).
                                                    DOMAIN
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PROSITE; PS50071; HOMEOBOX_2; 1.
Homeobox; DNA-binding; Developme
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PIR; S14932; S14932.
HSSP; P02833; 1SAN.
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Submitted (FEB-1998) t
                                                                                                                                         Transcription
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"Mutation of HOXA13 in hand-foot-genital syndrome.
"At. Genet. 15:179-180(1997).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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## ALIGNMENTS

homo sapien homo sapien

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Q PERSONAL PLANTS OF SELECTION 
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A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Welson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Sylistkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,

RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

Science 287:1185-2195(2000).

DR EMBL; AE003698; AAF54888.2:

DR FlyBase; FBgn0038108; CG7518.

DR FlyBase; FBgn0038108; CG7518.

DR FlyBase; FBgn0037; MYB_1; UNKNOWN_1.

SOURCE 2451 AA; 266959 MW; 088A2293F27481E2 CRC64;
                                                                                                             Matches
                                                                                                                                       Query Match
Best Local
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01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF315344; AAG42100.1; ...
MGD; MGI:1928323; Nisch.
InterPro; IPR001128; Cyt_P450.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
                                                                                                                                                                                                                                            PRINTS; PR00019; LEURICHRPT.

SMART; SM00370; LRR; 5.

PROSTIE; PS00086; CYTOCHROME_P450; UNKNOWN_1.

SEQUENCE 1354 AA; 148060 MW; 01BD676FDCA19247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alahari S.K., Lee J.W., Juliano R.L.;
"Nischarin, a Novel Protein That Interacts with the Integrin Subunit and Inhibits Cell Migration.";
J. Cell Biol. 151:1141-1154(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9EPW8;
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                                                     2 EAAAAAEAAAAEAAAAAEAAAAA
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EAPAAAEAPAAAEAPAAA
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                                                                                                                                    73.48;
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Last sequence update)
Last annotation update)
                                                                                                       Score 80; DB Pred. No. 2.2; 0; Mismatches
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Pred. No. 1.5;
0; Mismatches
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Best Local S
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Q9QXG2;
Q9QXG2;
01-MAY-2000 (
01-MAY-2000 (
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Q39598;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
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Q93WW0;
Q93WW0;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 10.7 KDA PROTEIN.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-92119224; PubMed-1731966;

MEDLINE-92119224; PubMed-1731966;

Makarchuk W.W., Muller F.W., Beck C.F.;

Makarchuk W.W. elements of Chlamydomonas reinhardtii with complex arrangements of directly repeated sequence motifs.*;

Plant Mol. Biol. 18:143-146(1992).

EMBL; X17208; CAA35080.1; -.
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NCBI_TaxID=3055;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
CGCR-4 PRODUCT (FRAGMENT).
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Submitted (AUG-2001) to the
EMBL; BC012681; AAH12681.1;
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TISSUE-SALIVARY GLAND;
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Submitted (DEC-1999) to the EMBL/G
EMBL; AF218084; AAF25478.1; "MGD; MGI:892979; Chm
InterPro; IPR002005; Rab_GDI_REP.
Pfam; PF00996; GDI; 1.
PFIMTS; PR00891; RABGDIREP.
SEQUENCE
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01-MAR-2001
01-DEC-2001
CDC2L5 PROTE
                                                                                  Pfam; PF00069; Pkinase; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00107; PROTEIN_KINASE_DOM; ATP-binding; Kinase; Transferase.

SEQUENCE 1452 AA; 158480 MW; C7ED0
                                                                                                                                                             InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                    Q9H4A0
Q9H4A0;
                                                                                                                                                                       Blochem. Blophys. Res. Commun. EMBL; AJ297710; CAC10401.1; -. HSSP; P24941; IBUH. InterPro; IPR000719; Euk_Pkina:
                                                                                                                                                                                                                                Marques F., Moreau J.L.,
Callebaut I.,
                                                                                                                                                                                                                                                      TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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Mammalia; Eutheria;
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CHOROIDEREMIA
                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                       "A new subfamily of high
                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
 463
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                                     l Similarity 79.2
19; Conservative
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19; Conser
                                                                                                                                                    IPR002290; Ser_thr_pkinase IPR001245; Tyr_pkinase.
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Metazoa; Chordata; C
----haria; Rodentia; (
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A; 73976 MW;
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Primates;
                                              79
                                                                                 Transferase.
158480 MW;
                                                                                                                                                                        Euk_pkinase
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79.2%;
                                              . 78;
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                                                                                                                                                                                                                       Perre E., molecular
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Perre E., Geneviere
                                                                                                                                                                                                                                                                                                                                      Created)
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the mouse choroideremia gene.";
EMBL/GenBank/DDBJ databases.
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                                             Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FF71A74AD3FBDEOA CRC64;
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                                      Mismatches
                                                                                C7ED072968B439CB CRC64;
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RESULT
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InterPro: IPR002290; Ser_thr_pkinase.
InterPro: IPR001245; Tyr_pkinase.
InterPro: IPR001245; Tyr_pkinase.
InterPro: IPR001245; Tyr_pkinase.
InterPro: IPR001245; Tyr.KC; 1.
SMARR; SM00219; S_TKC; 1.
SMARR; SM00219; Tyr.KC; 1.
SMARR; SM00219; Tyr.KC; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
ATP-bindang; Kinase; Transferase.
SEQUENCE 1512 AA; 164969 MW; 283B8D;
                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 0
01-MAY-1999 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
TROPOMYOSIN ISOFORM 33.
TM1 OR CG4898.
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O1-MAR-2001 (TrEMBLrel. 1
O1-MAR-2001 (TREMBLrel. 1
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CDC2L5 PROTEIN KINASE.
                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                  Q24426;
Q24426;
                  SEQUENCE FROM N.A.
MEDLINE=87064486; PubMed=3097506;
Karlik C.C., Fyrberg E.A.;
"Two Drosophila melanogaster tropomyosin
                                                                               "Organization of contractile protein ger of the D. melanogaster third chromosome. Cell 37:469-481(1984).
                                                                                                            SEQUENCE FROM N.A.
MEDLINE-84205681; Pubmed-6202423;
Karlik C.C., Mahaffey J.W., Coutu
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EMBL; AJ297709; CAC
HSSP; P24941; 1BUH.
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Homo sapiens (Human).
Homo sapiens (Human).
Thereas, Chordata,
Thereas, Primates;
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            functional
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19; Conser
l aspects.";
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Last sequence update)
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Catarrhini; Hominidae;
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; Homo.
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RESULT
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barla J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C. McLeod M.P., McPherson D.,
RA McNunt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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Matches 21
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InterPro; IPR002965; P_Tich_extensn.
InterPro; IPR002965; P_Tich_extensn.
InterPro; IPR00533; Tropomyosin.
Pfam; PF00261; Tropomyosin; 2.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01214; TROPOMYOSIN; 1.
PROSITE; PS00326; TROPOMYOSIN; 1.
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01-MAY-2000
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Q9VF97;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
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TM1 OR CG4898.
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L00358; AAA28968.1;
L00359; AAA28968.1;
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531 AA; 56047 MW;
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AAA28968.1;
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RESULT OF THE PROPERTY OF THE 
RX MEDLINE=20196006; PubMed=10731132;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galale R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galale R.F.,

RA Amanatides P.G., Scherer S.E., Ashburner M., Henderson S.N.,

RA Amanatides P.G., Kortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiifer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiifer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiifer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshkov S.,

RA Borkova D., Becchan M.R., Buuck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Hostin M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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Best Local S
Matches 21
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Q9VXD3;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
CG13012 PROT
CG13012;
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InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002395; P_pomyosin.
Pfam; PF00261; Tropomyosin; 2.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR00194; TROPOMYOSIN.
PROSITE; PS00326; TROPOMYOSIN; 1.
SEQUENCE 566 AA; 60449 MW; 2AF07CFB0DA2032E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Last annotation updat
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Pred. No. 2
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RESULT
OPERATE
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Brandon R.C., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Botshakov S.,
RA Gepalos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gepalos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dukov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liux X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy'M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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RA Mount S.M., Moy M., Murphy B., Murphy L.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Sher E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA VIITSKAS R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou Y., Shift H.O.,
RA Zheng X.H., Yhong F.N., Wolfin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
EMBL; AE003503; AAF48641.1;
DR EJYBase; FBgn003079; CC13012.
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Matches 18
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Etarygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-DEC-2001 (TrEMBLrel.
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Last annotation update)
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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Virskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
RThe genome sequence of Drosophila melanogaster.*;
Science 287:2185-2195(2000).
REMBL; AE003453; AAF46699.1; ...
RHSSP; 013625; 1YCS.
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InterPro; IPR002110; ANK.
InterPro; IPR00142; SH3.
Pfam; PF00023; ank; 2.
Pfam; PF00018; SH3; 1.
SMARR; SM00248; ANK; 2.
SMART; SM00326; SH3; 1.
PROSITE; PS50088; ANK_REPEAT; 2.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                   STRAIN-cwlfs MT;
STRAIN-cwlfs MT;
STRAIN-cwlfs MT;
MEDLINE-92119224; PubMed-1731966;
Makarchuk W.W., Muller F.W., Beck C.F.;
Makarchuk W.W. alements of Chlamydomonas reinhardtii with complex
"Two GC-Tich DNA elements of Chlamydomonas reinhardtii with complex
"Two GC-Tich DNA elements of directly repeated sequence mottifs.";
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01-NOV-1996
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Q39597;
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NON_TER
SEQUENCE
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Q9MAX9;
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Q1-CCT-2000 (TremBirel 15, C
Q1-CCT-2000 (TremBirel 15, I
Q1-DEC-2001 (TremBirel 19, I
SEQUENCE FROM N.A.
Finst R.J., Kim P.J., Griffis I
Fralp is a 171 kDa protein esse
in Chlamydomonas.;
J. Cell Sci. 0:0-0(2000).
FMBL; AF246990; AAF66419.1;
InterPro; IPR03592; LRR_out.
SMART; SM00370; LRR; 7.
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Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta;
Chlamydomonadaceae; Chlamydomonas.
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InterPro; IFR004089; Chemotaxis_transducer.
InterPro; IFR001611; LRR.
InterPro; IFR003592; LRR_out.
Pfam; PF00560; LRR; 5.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VARIABLE FLAGELLAR NUMBER PROTEIN.
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MEDLINE-21181843; Pubmed-11285274;
Silflow C.D., LaVoie M., Tam L.W.,
Borodovsky M., Lefebvre P.A.;
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"Cloning of flagellar genes
insertional mutagenesis.";
Genetics 135:375-384(1993).
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STRAIN-21GR, CC-1690;
MEDLINE-94063478; PubMed-8244002;
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InterPro; IPR001202; WW.
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SMART; SM00441; FF; 1.
SMART; SM00445; WW; 2.
SMART; SM00456; WW; 2.
PROSITE; PS01159; WW_DOMAIN_1; 1
PROSITE; PS50120; WW_DOMAIN_2; 2
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SEQUENCE 323 AA; 35148 MW; E
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Soluble peptide an Soluble tandem pEA Drosophila melanog Peptide #7868 enco Human brain expres Human bone marrow Peptide #8105 enco Novel human diagno Amino acid sequenc Drosophila melanog Urosophila melanog
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## ALIGNMENTS

PESULT AAB13781

AAB13781;

AAB13781 standard; peptide; 25

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10-NOV-2000 (first entry) Soluble peptide antigen pEA

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pEA peptide; cytostatic; vaccine; cytotoxic T cell; CTL; immunotherapy; major histocompatibility complex class 1; MHC class 1; antigen; tumour; prostate; breast; multiple myeloma.

Unidentified.

W0200035949-A1.

22-JUN-2000.

14-DEC-1999; 99WO-US29724.

14-DEC-1998; 98US-0112324.

(DEND-) DENDREON CORP.

Laus R, Hakim I, Vidovic D;
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Antigens modified by the covalent addition of a peptide that facilitates entry into antigen presenting cells, useful for producing compositions for immunizing against tumors and pathogens -  $\frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \int_$ 

WPI; 2000-442365/38.

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                                                                                                                    The present invention relates to compositions of modified soluble protein antigens capable of eliciting an enhanced in vivo cytotoxic T cell (CTL) response i.e. a major histocompatability complex (MHC) class I molecule response. The protein antigen is modified by the covalent addition of a peptide sequence which facilitate entry of the antigen into antigen peptide sequence which facilitate entry of the antigen into antigen sequence which can be used to modify the soluble antigens. The present sequence is tandem pEA/ pK peptide conjugate. The modified antigen composition may be used for immunising against, or treating a tumour e.g.
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major histocompatibility complex class 1; MHC class 1; antigen; tumour
prostate; breast; multiple myeloma; pEA peptide.
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Pred. No. 1.8e-07;
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                                                                                                                          capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                        The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                     Disclosure; SEQ ID NO 41514; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
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              Local
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Score 84; DB
Pred. No. 0.02
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ABB40362
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                                                                                                                                                                                                       RESULT
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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03-AUG-2000;
21-SEP-2000;
     Human; brain expressed exon; gene microarray; Alzheimer's disease; m
                                                         Human brain expressed single
                                                                                                                                  AAM61172;
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26-MAY-2000; 2000US-0207456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome-derived single exon nucleic acid probes useful for ting gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; SEQ ID NO 32997; 639pp + sequence listing; English
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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e expression analysis; probe;
multiple sclerosis; schizophrenia;
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04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
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27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                          Human; bone marrow expressed exon; gene expression analysis; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                    30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and imputed treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
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brains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of single exon nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epilepsy; cancer
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; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
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2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
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2000US-0236359
2000US-0236353
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Pred. No. 0.0043;
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                                                                                                                                                                                                                           probe;
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Best Local :
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                            Penn
                                                                                                                                                                                  30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                 genetic disorder
                                                                                                                                                                                                                                                                           Probe; microarray; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                (MOLE-)
                                                                                                                                                                                                                          WO200157272-A2
                                                                                                                                                                                                                                               Homo
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                                                                                                                                                                                                                                                                                               Peptide #8105 encoded
                                                                                                                                                                                                                                                                                                                                        AAM34068
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                                       2001-488897/53.
                                                                                                                                                                                                                                              sapiens
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       genome-derived single exon nucleic acid zing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome-derived single exon nucleic acid probes useful for
zing gene expression in human bone marrow -
                                                                                MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                            Hanzel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO: 34192;
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2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                           Protein; 119
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                                                          Chen
                                                                                                                                                                                                                                                                                               by probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                          placenta; antenatal diagnosis
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Pred. No.
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The invention relates to isolated polynucleotide (I) and C polypeptide (II) sequences. (I) is useful as hybridisation probes, C polypeptide chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The C polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating classing of sites expressing (II). (I) and (II) are useful for treating the polypeptide and polypucleotide sequences have applications in the polypeptide and polypucleotide sequences have applications in
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Best Local
                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000;
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2000US-0649167
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                A cDNA library constructed from foetal ganglioside mRNA was screened with a butyryl-cholinesterase (bCh) cDNA probe to identify one clone (clone 14) contg. about 250 bases at the 5'-region of the bCh coding sequence plus a sequence which hybridised with genomic DNA from patients with acute myelocytic leukaemia. AAP95268 is the translation of the upper reading frame and is claimed in the patent. Its nucleic acid can be isolated, opt. together with its signal sequence, by screening cDNA or genomic libraries with the clone 14 DNA, to identify a full-length clone. The material from this clone can be transferred into mammalian or microbial host cells and these cultured for its prodn. It has hormonal activity in modulation of haematopoiesis and immune responses. It is useful in standard immunoassy or hybridisation procedures for the production and diagnosis of rare leukaemias. It may also be useful
                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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JP03195496-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hermona S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (YISS ) YISSUM RES DEV CO
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1991-292630/40
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leukaemia diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                             7; Page 17; Fig 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              haematopoiesis and immune response, and der
d, antibodies, etc., useful eg in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haim Z;
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Pred. No. 0.00
0; Mismatches
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Query Match Best Local S Matches 21

Similarity

69.3%; 87.5%;

Conservative

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Score 75.5; DB Pred. No. 0.054; 0; Mismatches

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                The sequence data for this patent did not form specification, but was obtained in electronic fat ftp.wipo.int/pub/published_pct_sequences.
                                                            capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
Sequence
                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                         Disclosure; SEQ ID NO
                                                                                                                                                                                        New isolated nucleic genes from Drosophila
                                                                                                                                                                                interactions
                                                                                                                                                                                                                            N-PSDB; ABL05143.
                                                                                                                                                                                                                                        WPI; 2001-656860/75
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                                                      ABB57737-ABB72072
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79.28;
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Pred. No.
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RESULT 1
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Best Local :
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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                            Human secreted
                                                    06-OCT-2000
                                                                           AAG00758
                                                                                                AAG00758 standard;
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 29862; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 genes from Drosophila and for elucidating cell signalling and c
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N-PSDB; ABL11793.
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11-JUL-2000;
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18; Conser
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                                                                                                                                                                                                                                                                  221 AA;
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                                                                                                                                                                                                       Conservative
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                                                  (first entry)
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2000US-0614150.
                            protein,
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81.8%;
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Pred. No. 0.
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                                                                                                                                                                                                       Mismatches
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RESULT 13
AAW22875
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Best Local Similarity 86.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                       30-JAN-1997;
                                                                          WO9728260-A1
                                                                                                  Pseudopleuronectus americanus
                                                                                                                                     Antifreeze polypeptide; intracellular skin type AFP; winter flounder;
                                                                                                                                                                     P. americanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                07-AUG-1997
                                                                                                                               cold
                                                                                                                                                                                               23-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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DB; AAC00764.
                                                                                                                            resistance;
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                                                                                                                                                                                            (first entry)
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                                                                                                                                                                  skin type antifreeze polypeptide. sAFP8
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                       97WO-CA00062
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                                                                                                                           thermal hysteresis; antibacterial
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86.4%;
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Pred. No. 0.045;
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31-JAN-1996;

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ABG18917
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Best Local
New isolated polynucleotide and encoded polypeptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the sAFP8 clone corresponding to a novel skin intracellular antifreeze polypeptide (AFP) which induces a concentration dependent decrease in the freezing point of an aqueous solution. This novel polypeptide does not contain a signal sequence and is thought to be intracellular. AFP's can be used to make an aqueous composition resistant to freezing by changing its thermal hysteresis such as a water or salt solution, an intracellular compartment of a cell or a food stuff, e.g. recrystalisation during cold storage, improving the texture and palatability of the food and has antibacterial properties. Such polypeptides can also be expressed to provide cold resistance to cells, e.g. plant, fungal animal or bacterial cells. The antibodies can be used to identify and isolate AFP while its promotter can be used to direct expression of a nucleic acid.
                               WPI; 2001-639362/73
N-PSDB; AAS83104.
                                                                         Drmanac RT,
                                                                                                                                31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated fish skin anti-freeze polypeptide - useful to depress freezing points of aqueous compositions and protect plant, funanimal or bacterial cells from cold
                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                           30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                        11-OCT-2001
                                                                                                                                                                                                                                    WO200175067-A2
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #18908
                                                                                                                                                                                                                                                                                                                                                                18-FEB-2002
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N-PSDB; AAT75505.
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                                                                                                                                2000US-0540217
2000US-0649167
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RESULT 15
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Note: The sequence data for this pattent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at first, wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                          WPI; 2001-656860/75
N-PSDB; ABL04682.
                                                                                                                       (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                   W0200171042-A2
                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 8529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostics, forensics, responsible for genetic biodiversity
                                                                                                                                                                     23-MAR-2000;
                                                                                                                                                                                                   23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                 pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation
                                                                                                                                                        11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB60579 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20;
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2000US-0614150
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Pred. No. 0.083;
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New isolated nucleic acid genes from Drosophila and

detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell

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                                                                                                В
                                                                                                                                                                         Query Match 66.1%; Score 72; DB 22; Best Local Similarity 79.2%; Pred. No. 0.28; Matches 19; Conservative 0; Mismatches 5
                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG1840-ABLIG175) and the encoded proteins (ABB5737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 8529; 21pp + Sequence Listing; English.
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                                                                                            1071 AA;
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Copyright (c) 1993 - 2000 Com
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## ALIGNMENTS

A:Cross-references: GB:M19057; NID:g324210 A:Note: the sequence in GenBank entry FLAH: C:Genetics: A; Molecule type: genomi A; Residues: 1-550 <KID> C.Superfamily: influenza virus hemagglutinin
C.Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolest
F;1-328/Product: hemagglutinin HA1 #status predicted <HA1>
F;30-550/Product: hemagglutinin HA2 #status predicted <HA2>
F;520-36/Domain: transmembrane #status predicted <MM1>
F;820-38.165,285,483/Binding site: carbohydrate (Asn) (covalent) #status
F;14-466,52-277,64-76,139-473,281-305/Disulfide bonds: #status predicted
F;539,546,549/Binding site: palmitate (Cys) (covalent) #status predicted 망 A;Molecule type: genomic RNA A;Residues: 1-550 <KID> A;Cross-references: GB:M19056; NID:g324208 A;Note: the sequence in GenBank entry FLAHAPA, C;Genetics: Ş C;Accession: A29971
R;Kida, H.; Shortridge, K.F.; Webster, R.G. C;Species: influenza A virus C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 18-Sep-1998 Virology 162, 160-166, 1988
A;Title: Origin of the hemagglutinin gene of H3N2 influenza viruses from pigs in Chir A;Reference number: A94370; MUID:88101364
A;Accession: A29971 HMIVS3 A; Map position: segment 4 HMIVS2 RESULT nemagglutinin precursor - influenza A virus (strain A/swine/126/82) (fragment) Matches Query Match Best Local 330 Local N sequence in GenBank entry FLAHAPB, l Similarity 100 23; Conservative genomic RNA 93.7%; Score 134; DB 1; L; Pred. No. 1.4e-10; 352 release 106, (PID:g324209) differs Length 550; Indels 0 thiolester Gaps pigs in predicted bond 0 frc

release 106, (PID:g324211) differs

frc

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N:Contains: hemagglutinin HA1; hemagglutinin HA2
C:Species: influenza A virus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #te
C:Accession: B27813
R:Kida, H.; Kawaoka, Y.; Naeve, C.W.; Webster, R.G.
Virology 159, 109-119, 1987
A:Title: Antigenic and genetic conservation of H3 infl
A:Reference number: A94363; MUID:87265458
A:Accession: B27813
A:Molecule type: genomic RNA
A:Residues: 1-550 <KID>
A:Crcss-references: GB:M16738; NID:g324083
A:Note: the translation in Fig. 2 is inconsistent with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Map position: segment 4
C:Superfamily: infileenza virus hemagglutinin
C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester
F:1-328/Product: hemagglutinin HAI *status predicted <HAI>
F:330-550/Product: hemagglutinin HA2 *status predicted <HA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hemagglutinin precursor - influenza A virus (strain A/duck/Hokkaido/5/77) (fragment) N;Contains: hemagglutinin HA1; hemagglutinin HA2 C;Species: influenza A virus C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999 C;Accession: A27813 C;Accession: A27813 R;Kida, H.; Kawaoka, Y.; Naeve, C.W.; Webster, R.G. Virology 159, 109-119, 1987
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C:Superfamily: influenza virus hemagglutinin
C:Keywords: glycoprotein: hemagglutinin: homotrimer; lipoprotein; thiolest
F:1-328/Product: hemagglutinin HA1 *status predicted <HA1>
F:300-550/Product: hemagglutinin HA2 *status predicted <HA2>
F:300-550/Product: hemagglutinin HA2 *status predicted <HA2>
F:520-535/Domain: transmembrane *status predicted <TMI>
F:8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) *status
F:14-466,52-277,64-76,139-473,281-305/Disulfide bonds: *status predicted
F:14-466,52-277,64-76,139-473,281-305/Disulfide bonds: *status predicted
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F;8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status F;8,22,38,165,285,483/Binding site: carbohydrate bonds: #status predicted F;14-466,52-277,64-76,139-473,281-305/Disulfide bonds: #status predicted F;539,546,549/Binding site: palmitate (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Antigenic and genetic conservation of H3 influenza virus A;Reference number: A94363; MUID:87265458 A;Accession: A27813
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N:Contains: hemagglutinin HA1; hemagglutinin HA2
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A; Residues: 1-550 <KID>
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100.0%; Pr
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                                       NID:g324083 . 2 is inconsistent with
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Pred. No. 1.4e-10;
0; Mismatches 0;
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                                    nucleotide sequence
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                                 Fig.
C;Genetics:
A;Map position: segment 4
                                                                                                                              C;Accession: D27813
R;Kida, H.; Kawaoka, Y.; Naeve, C.W.; Webster, R.G. Virology 159, 109-119, 1987
A;Title: Antigentc and genetic conservation of H3 1 A;Reference number: A94363; MUID:87265458
A;Accession: D27813
                                                                                                                                                                                                                                                                                  N:Contains: hemagglutinin HA1; hemagglutinin HA2
C:Species: influenza A virus
C:Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
                                                                              A; Molecule type: genomic RNA
A; Residues: 1-550 <KID>
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                                                        A; Cross-references: GB:M16740;
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330 GLFGAIAGFIENGWEGMIDGWYG

352 24

NID: g324087; PIDN: AAA43146.1;

PID: 9324088

H3 influenza

virus

'n

wild ducks

A/duck/Hokkaido/7/82) (fragment

2 GLFGAIAGFIENGWEGMIDGWYG

Local Similarity

93.7%; ilarity 100.0%; Conservative

Score 134; DB 1; I pred. No. 1.4e-10; pred. No. 1.4e-0;

Length 550;

predicted

bond

Indels

0

Gaps

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C:Superfamily: influenza virus hemagglutinin
C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester
F:1-328/Product: hemagglutinin HA1 *status predicted <HA1>
F:300-550/Product: hemagglutinin HA2 *status predicted <HA2>
F:500-536/Domain: transmembrane *status predicted <MM1>
F:520-536/Domain: transmembrane *status predicted <MM1>
F:80.23.38,165,285,483/Binding site: carbohydrate (Asn) (covalent) *status predicted
F:14-466,52-277,64-76,139-473,281-305/Disulfide bonds: *status predicted
F:539,546,549/Binding site: palmitate (Cys) (covalent) *status predicted
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C; Superfamily: influenza virus hemagglutinin
C; Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester
F; 1-328/Product: hemagglutinin HAI *status predicted <HAI>
F; 330-550/Product: hemagglutinin HA2 *status predicted <HAI>
F; 330-550/Product: hemagglutinin HA2 *status predicted <TMI>
F; 520-536/Domain: transmembrane *status.predicted <TMI>
F; 8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) *status predicted
F; 14-466,52-277,64-76,139-473,281-305/Disulfide bonds: *status predicted
F; 339,546,549/Binding site: palmitate (Cys) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kida, H.; Kawaoka, Y.; Naeve, C.W.; Webster, R.G. Virology 159, 109-119, 1987
A;Title: Antigenic and genetic conservation of H3 influenza virus A;Reference number: A94363; MUID:87265458
A;Accession: C27813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hemagglutinin precursor - influenza A virus (strain A/duck/Hokkaido/33/80) (fragmen N;Contains: hemagglutinin HA1; hemagglutinin HA2 C;Species: influenza A virus C;Species: influenza A virus C;Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                           A; Map
                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M16739; NID:g324085; PIDN:AAA43145.1; PID:g324086
                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: genomic RNA
A; Residues: 1-550 <KID>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: C27813
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100.0%; Pr
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; Pred. No. 1.4e-10;
0; Mismatches 0;
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hemagglutinin precursor - influenza A virus (strain A/duck/Hokkaido/9/85) (fragment) N:Contains: hemagglutinin HA1; hemagglutinin HA2 C;Species: influenza A virus C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Sep-1998 C;Accession: F27813 R;Kida, H.; Kawaoka, Y.; Naeve, C.W.; Webster, R.G. Virology 159, 109-119, 1987 A;Title: Antigenic and genetic conservation of H3 influenza virus in wild ducks. A;Recession: F27813 A;Molecule type: genomic RNA A;Recession: F27813 A;Molecule type: genomic RNA A;Residues: 1-550 <KID>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: segment 4
C; Superfamily: influenza virus hemagglutinin
C; Keywords: glycoprotein: hemagglutinin; homotrimer
F; 1-328/Product: hemagglutinin HA1 *status predicted <HA1>
F; 330-550/Product: hemagglutinin HA2 *status predicted <HA2>
F; 320-550/Domain: transmembrane *status predicted <TM1>
F; 7.8, 22, 38, 165, 285, 483/Binding site: carbohydrate (Asn) (covalent) *status predicted F; 14-466, 52-277, 64-76, 139-473, 281-305/Disulfide bonds: *status predicted
A;Cross-references: GB:M16742; NID:g324091
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
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HMMV21
HMMV21
HMMV21
Hemagglutinin precursor - influenza A virus (strain A/duck/Hokkaido/21/82) (fragment)
Hemagglutinin precursor - influenza A virus
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C.Species: influenza A virus
C.Date: 30-un-1989 #sequence_revision 30-Jun-1989 #text_change 18-Sep-1998
C.Accession: E27813
R.Kida, H.; Kawaoka, Y.; Naeve, C.W.; Webster, R.G.
Virology 159, 109-119, 1987
A:Title: Antigenic and genetic conservation of H3 influenza virus in wild ducks.
A:Reference number: A94363; MUID:87265458
A:Accession: E27813
A:Molecule type: genomic RNA
A:Residues: 1-550 <KIDD
A:Const: 1-550 <KIDD
A:Const: references: GB:M16741; NID:g324089
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C:Keywords: 91ycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester
F:1-328/Froduct: hemagglutinin HA1 *status predicted <HA1>
F:330-550/Product: hemagglutinin HA2 *status predicted <HA2>
F:520-536/Domain: transmembrane *status predicted <MM1>
F:8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) *status predicted F:14-466,52-277,64-76,139-473,281-305/Disulfide bonds: *status predicted F:539,546,549/Binding site: palmitate (Cys) (covalent) *status predicted
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A; Molecule type: genomic RNA
A; Residues: 1-550 < YAS>
A; Cross-references: GB: D00929; NID: g221279; PID
A; Cross-references: GB: D00929; NID: g221279; PID
A; Note: the authors translated the codon GGG fo
A; Note: residues 528-532 are not shown in this
C; Superfamily: influenza virus hemagglutinin
C; Keywords: glycoprotein; homotrimer
F; 1-328/Product: hemagglutinin HA1 #status pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolest F;1-388/Product: hemagglutinin HA1 *status predicted <HA1> F;330-550/Product: hemagglutinin HA2 *status predicted <HA2> F;520-536/Domain: transmembrane *status predicted <TMI> F;8.22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) *status F;14-466,52-277,64-76,139-473,281-305/Disulfide bonds: *status predicted F;539,546,549/Binding site: palmitate (Cys) (covalent) *status predicted
                                                                                                                                                                                                     R; Yasuda, J.; Shortridge, K.F.; Shimizu, Y
J. Gen. Virol. 72, 2007-2010, 1991
A;Title: Molecular evidence for a role of
A;Reference number: JQ1153; MUID:91341491
A;Accession: JQ1153
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Best Local Similarity
"~+~hes 23; Conserv
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F:330-550/Product: hemagglutinin HA2 *status predicted <HA2>
F:530-536/Domain: transmembrane *status predicted <TM1>
F:8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) *status F:14-466,52-277,64-76,139-473,281-305/Disulfide bonds: *status predicted F:539,546,549/Binding site: palmitate (Cys) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                              C;Species: influenza A virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
C;Accession: JQ1153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hemagglutinin precursor - influenza A virus (strain A/duck/Hokkaido/10/85) (fragment) N; Contains: hemagglutinin HA1; hemagglutinin HA2 C; Species: influenza A virus
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C;Superfamily: influenza virus hemagglutinin
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A; Residues: 1-550 <KID>
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A;TILLe: Antigenic and genetic conservation
A;Reference number: A94363; MUID:87265458
A;Accession: G27813
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Contains: hemagglutinin HA1; hemagglutinin HA2
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llarity 100.0%;
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                                                                                                                             NID: g221279; PIDN: BAA00769.1;
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Pred. No. 1.4e-10;
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Pred. No. 1.4e-10;
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hemagglutinin HA1 #status predicted <HA1>

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A;Cross-references: GB:D00931; NID:g221277; PIDN:BAA00771.1; PID:g221278 A;Note: the authors translated the codon GGG for residue 218 as Glu, GCC f A;Note: residues 528-532 are not shown in this publication C;Superfamily: influenza virus hemagglutinin C;Superfamily: influenza virus hemagglutinin C;Superfamily: influenza virus hemagglutinin C;Superfamily: hemagglutinin HA1 #status predicted <HA1>F;330-545/Product: hemagglutinin HA2 #status predicted <HA2>F;830-545/Product: hemagglutinin HA2 #status predicted <HA2>F;8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status
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R;Yasuda, J; Shortridge, K.F.; Shimizu, Y.; Kida, H.
J. Gen. Virol. 72, 2007-2010, 1991
A;Title: Molecular evidence for a role of domestic ducks in the introduction of avian A;Reference number: JO1153; MUID:91341491
A;Rocession: JO1154
A;Molecule type: genomic RNA
A;Residues: 1-550 <YAS>
A;Residues: 1-550 <YAS>
A;Rote: the authors translated the codon GGG for residue 218 as Glu
A;Note: residues 528-532 are not shown in this publication
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; homotrimer
F;1-338/Product: hemagglutinin HA1 #status predicted <HA1>
F;330-545/Product: hemagglutinin HA2 #status predicted <HA2>
F;8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status predicted
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J. Gen. Virol. 72, 2007-2010, 1991
A;Title: Molecular evidence for a role of domestic ducks in the introduction A;Reference number: JQ1153; MUID:91341491
A;Accession: JQ1155
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A; Residues: 1-550 < YAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Jun-2000 C;Accession: JQ1155
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C;Date: 31-Mar-1992 #sequence
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N;Contains: hemagglutinin HA1; hemagglutinin HA2
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                                                             Qwiery Match
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Best Local Similarity 100.0%;
Matches 23; Conservative
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          Conservative
                             93.7%;
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          0,
                             Score 134; DB 2;
Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 134; DB 2;
; Pred. No. 1.4e-10;
0; Mismatches 0;
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Pred. No. 1.4e-10;
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                                                  Length 550
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                                                                                                                          predicted
  0;
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A; Residues: 1-566 < VER>
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A; Residues: 1-566 <BOT>
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23; Conservative
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N;Contains: hemagglutinin HAI; hemagglutinin HAZ
C;Species: influenza A virus
C;Date: 19-May-1994 *sequence_revision 19-May-1994 *text_change 16-Jul-1999
C;Accession: A93231; A04051
R;Verhoeyen, M.; Fang, R.; Min Jou, W.; Devos, R.; Huylebroeck, D.; Saman, E Mature 286, 771-776, 1980
A;Title: Antigenic drift between the haemagglutinin of the Hong Kong influer A;Reference number: A93231; MUID:80254693
A;Accession: A93231
A;Cross references: GB:J02090; NID:g324131; PIDN:AAA43178.1; PID:g3:C;Superfamily: influenza virus hemagglutinin (C;Keywords: hemagglutinin; homotrimer; lipoprotein; thiolester bond F;1-16/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: strain x-31[H3]
(;Superfamily: influenza virus hemagglutinin
(;Keywords: hemagglutinin; homotrimer; lipoprotein; thiolester
F;1-16/Domain: signal sequence #status predicted <KA1>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;346-566/Product: hemagglutinin HA2 #status predicted <HA2>
F;346-525/Domain: transmembrane #status predicted <TM1>
F;30-482,68-293,80-92,155-489,297-321/Disulfide bonds: #status
F;555,562,565/Binding site: palmitate (Cys) (covalent) #status
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R:Dopheide, T.A.; Ward, C.W.
A:Title: The disulphide bonds of a Hong Kong influenza virus hemagglutinin. A:Reference number: A91276; MUID:80179105
A:Contents: annotation; disulfide bonds
A:Gething, M.J.; Bye, J.; Skehel, J.; Waterfield, M.
Nature 287, 301-306, 1980
A:Title: Cloning and DNA sequence of double-stranded copies of haemagglutinin A:Reference number: A93233; MUID:81030852
A:Accession: A93233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Both, G.W.; Sleigh, M.J.
Nucleic Acids Res. 8, 2561-2575, 1980
A;Title: Complete nucleotide sequence of the haemagglutinin
A;Reference number: A93705; MUID:81053698
A;Accession: A93705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: genomic RNA
A; Residues: 1-24,'S',26,'D',28-159,'G',161-197,'I',199-241,'L',243-249 <GETY
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C;Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hemagglutinin precursor - influenza A virus (strain A/Aichi/2/68
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                                                                                                                 NID: g324131; PIDN: AAA43178.1; PID: g324132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 134; DB 1; Pred. No. 1.4e-10; Operations 0;
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hemagglutinin precursor influenza A virus (strain A/Mem/102/72)

N;Contains: hemagglutinin HAI; hemagglutinin HAZ

C;Species: influenza A virus

C;Accession: A94441; A04051

R;Sleigh, M.J.; Both, G.W.; Brownlee, G.G.; Bender, V.J.; Moss, B.A.

in Structure and Variation in Influenza Virus, Laver, G., and Air, G., eds., pp. 69-79, E

A;Title: The haemagglutinin gene of influenza A virus: nucleotide sequence analysis of c

A;Reference number: A94441

A;Accession: A94441

A;Accession: A94441

A;Molecule type: genomic RNA

A;Residues: 1-566 <SLE>
C;Superfamily: influenza virus hemagglutinin

C;Keywords: hemagglutinin; homotrimer; lipoprotein; thiolester bond

F;1-16/Domain: signal sequence *status predicted <HAI>
F;346-566/Product: hemagglutinin HAI *status predicted <HAI>
F;355,562,565/Binding site: palmitate (Cys) (covalent) *status predicted
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Search completed: July 1, 2002, 06:28:11 Job time: 713 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMA_TADH2 STANDARD; PRT; 550 AA. P12583; Q84011; O1-CCT-1989 (Rel. 12, Created) O1-A-RR-1990 (Rel. 14, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) Hemagglutinin precursor [Contains: Hemagglutinin HA2 chain] (Fragment).
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ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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MEDLINE-87265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Influenza A virus (strain A/Duck/Hokkaido/8/80).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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CELL RECEPTORS AND FOR INITATING INFECTION.
SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO
(HA1 AND HA2) LINKED BY A DISCLFIDE BOND.
SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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Influenza A virus (strain A/Duck/Hokkaido/7/82)
Viruses; ssRNA negative-strand viruses; Orthomy
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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Influenza A virus (strain A/Duck/Hokkaido/21/82).
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-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-87265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster F
"Antigenic and genetic conservation of H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Influenza
Influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000225;
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m; PD000225; Hemagglutn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M16740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
  159:109-119(1987)
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Pred. No. 1.1e-10;
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                                                       Webster R.G
                                      of H3 influenza
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influenza virus
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Best Local S
Matches 23
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ProDom; PD000225; Hemagglutin; 1.

Envelope protein; Hemagglutinin; NON_TER 1
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                                                                                                                                                                                                                       ducks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza A virus (strain A/Duck/Hokkaido/9/85).
Viruses: ssRNA negative-strand viruses: Orthomyx
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-i- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
                                                                                                                                                                               Virology
                                                                                                                                                                                                                                               MEDLINE-87265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W.,
"Antigenic and genetic conservati
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=11362;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Influenza virus A and Influenza A virus.
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HSSP; P03437; 5HMG.
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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             FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING CELL RECEPTORS AND FOR INITIATING INFECTION. SUBUNIT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED E (HA1 AND HA2) LINKED BY A DISULFIDE BOND. SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FA
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HEMAGGLUTININ HAZ CHAIN.
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N-LINKED (GLCNAC. .) (PO
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             INFLUENZA HEMAGGLUTININ FAMILY
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ion of H3 influenza virus in
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                                                                                                                                                             Virology 159:109-119(1987).

-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VCELL RECEPTORS AND FOR INITIATING INFECTION.

-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO (HA1 AND HA2) LINKED BY A DISULFIDE BOND.

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-87265458; Pubmed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMA_IADH7 STANDARD; PRT; 550 AA. P1258; Q844018; Q89470; 01-QCT-1989 (Rel. 12, Created) 01-QCT-1989 (Rel. 12, Last sequence update) 16-QCT-2001 (Rel. 40, Last annotation update) Hemagglutinin precursor [Contains: Hemagglutinin HA2 chain] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
            EMBL;
                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                         entities requires a license agreement (See http://www.isb-sib.cr send an email to license@isb-sib.ch).
                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                           "Antigenic and genetic conservation
ducks.";
                                                                                                                                                                                                                                                                                                                                                  Influenza virus A Influenza A virus. NCBI_TaxID=11363;
                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA negative-strand viruses; Orthomyxovi
Influenza virus A and B group; Influenza A viruses;
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IPR001364; Hemagglutn.
0509; Hemagglutinin; 1.
                                                                                                                                                                                                                                                                                                                                                                                             A virus (strain A/Duck/Hokkaido/10/85).
ssRNA negative-strand viruses; Orthomyxoviridae;
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HEMAGGLUTININ HA2 CHAIN.
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Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
"Molecular evidence for a role of domestic ducks in the introduction of avian H3 influenza viruses to pigs in southern China, where the A/Hong Kong/68 (H3N2) strain emerged.";
J. Gen. Virol. 72:2007-2010(1991).
-i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
                                                                                                              InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutnin; 1.
ProDom; PP0000225; Hemagglutn; 1.
Envelope protein; Hemagglutnin; Glycoprotein.
                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin HAl chain;
Hemagglutinin HA2 chain] (Fragment).
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SEQUENCE
                                                                                                                                                                                                        EMBL; D00929; BAA00769.1; HSSP; P03437; 5HMG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY
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RESULT 9
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OX Influenza A
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InterPro: IPR001364; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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"Molecular evidence for a role of domestic ducks
of avian H3 influenza viruso + -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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J. Gen. Virol. 72:2007-2010(1991)
-1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS CELL RECEPTORS AND FOR INITIATING INFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D00931; BAA00771.1; HSSP; P03437; 2HMG.
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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Influenza A virus.
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
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in HA2 chain) (Fragment).
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HEMAGGLUTININ HA2 CHAIN.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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Wolecular evidence for a role of domestic ducks in the introduction of avian H3 influenza viruses to pigs in southern China, where the A/Hong Kong/68 (H3N2) strain emerged.";

J. Gen. Virol. 72:2007-2010(1991).

-I. FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.

-I. SUBUNIT: HOMOTRIMER. EACH OF THE MONOWERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin HA2 chain] (Fragment).
                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                           Envelope protein; Hemagglutinin; Glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Influenza A virus (strain A/Goose/Hong Kong/10/76).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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HEMAGGLUTININ HA2 CHAIN.
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RESULT 11 HEMA\_IAZH2

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Best Local :
                                      HEMA_IAZH3 STANDARD; PRT; 550 AA P11134; Q84025; Q84026; 01-JUL-1989 (Rel. 11, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hemagglutinin (Contains: Hemagglutinin HAI chain) (Fragment).
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CARBOHYD
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In China.";
Virology 162:160-166(1988).

-i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR AT CELL RECEPTORS AND FOR INITIATING INFECTION.

-i- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS (HAI AND HA2) LINKED BY A DISULFIDE BONDS.

(HAI AND HA2) LINKED BY A DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001364; Hemagglutn. Pfam; PF00509; Hemagglutinin; 1. ProDom; PD000225; Hemagglutn; 1. Hemagglutinin; Envelope protein;
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SEQUENCE FROM N.A.
MEDLING-88101364; PubMed-3336940;
Kida H., Shortridge K.F., Webster R.G.;
Kida H., Shortridge K.F., Webster R.G.;
                                                                                                                                                    IAZH3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1989 (Rel. 11, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat Hemagglutinin (Contains: Hemagglutinin HA)
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P11133; Q84019; Q84020;
01-JUL-1989 (Rel. 11, Cr
                  Influenza
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    SSRNA
A virus (strain A/Swine/Hong Kong/126/82).
ssRNA negative-strand viruses; Orthomyxovir
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                                                    MEDLINE-80254693; PubMed-7402351; MEDLINE-80254693; PubMed-7402351; Min Jou W.,
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SEQUENCE
   Verhoeyen M., Fang R.,
Saman E., Fiers W.;
"Antigenic drift between
                                                                                                                                                                                                                                   Viruses; ssRNA negative-strand viruses; Orthomyxovi
Influenza virus A and B group; Influenza A viruses;
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Influenza A virus.
NCBI_TaxID=150147;
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                                                                                                                                                                                                                                                                                                Influenza A virus
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-1- SUBBUNT: HOMOTRINER. EACH OF THE MONOMERS IS FORMED (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
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Virology 162:160-166(1988)
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P03437; 1PR001364; Hemagglutn.
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protein; Glycoprotein.
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EMBL; J02090; AAA43178.1; -
EMBL; V01085; CAA24269.1; -
PIR; A93231; HMIVHA.
PDB; 2HMG; 31-OCT-93.
PDB; 3HMG; 31-OCT-93.
PDB; 5HMG; 31-JAN-94.
PDB; 1HGD; 31-JAN-94.
PDB; 1HGE; 31-JAN-94.
PDB; 1HGF; 31-JAN-94.
PDB; 1HGF; 31-JAN-94.
PDB; 1HGG; 31-JAN-94.
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Fleury D., Wharton S.A., Skehel J.J., Knossow M., Bizebard T.;
"Antigen distortion allows influenza virus to escape neutralization Nat. Struct. Biol. 5:119-123(1998).

-i. FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS CELL RECEPTORS AND FOR INTIATING INFECTION.

-i. SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAI (HAI AND HA2) LINKED BY A DISULFIDE BOND.
                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-94352388; PubMed-8072525;
Bullough P.A., Hughson F.M., Skehel J.J.,
"Structure of influenza haemagglutinin at
"Structure 371:37-43(1994).
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J. Mol. Biol. 212:737-761(1990).
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MEDLLINE=90330310; PubMed=2329580;

Wels W.I., Bruenger A.T., Skehel J.J., Wiley D.C.;

"Refinement of the influenza virus hemagglutinin by simulated annealing.";
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Wiley D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-81123029; PubMed-7464906; Wilson I.A., Skehel J.J., Wiley D.C.; "Structure of the haemagitatinin membrane glycoprotein of influenza virus at J-A resolution."; Nature 289:366-373(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
[2]
                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (3.25 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                       "The structure of a membrane haemagglutinin."; EMBO J. 9:17-24(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure of the influenza virus haemagglutinin complexed with receptor, sialic acid."; Nature 33:426-431(1988).
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J.H., Cusack S.C.,
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escape neutralization.";
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H of membrane fusion.";
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ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin;
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29-APR-98.
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RESULT 13
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ID HEMAAIA
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01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin HA2 chain].
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P26134;
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J. Virol. 66:1129-1138(1992)
-I- FUNCTION: HEMAGGLUTININ
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MEDLINE-92114135; PubMed-1731092;
Bean W.J., Schell M., Katz J., Ka
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Webster R.G.;
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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Best Local
                                               EMBL; V01087; CAA24271.1; -
PIR; A04053; HMIVDU.
TnterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P03442;
21-JUL-1986
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                 MEDLINE=82025542; PubMed=6169439;
Fang R., Min Jou W., Huylebroeck D., Devos R., Fiers W.;
"Complete structure of A/duck/Ukraine/63 influenza hemagglutiningene: animal virus as progenitor of human H3 Hong Kong 1968 influ
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin Hemagglutinin Haz chain].
                                                                                                                                                                                                                                                                                                         hemagglutinin.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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ProDom; PD000225; Hemagglutn; 1.
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                                                                                                                                                                                                                       FUNCTION: HÉMAGGÉUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS CELL RECEPTORS AND FOR INITIATING INFECTION.
SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAI (HAI AND HA2) LINKED BY A DISULFIDE BOND.
SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                           25:315-323(1981)
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	arch completed: July 1, 2002, 0	Qy 2 GLFGAIAGFIENGWEGMIDGWYG 24	Query Match 93.7%; Score 134; DB 1; Length 566; Best Local Similarity 100.0%; Pred. No. 1.1e-10; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FT CHAIN  17 344 HEMAGGLUTININ HAI CHAIN.  FT CHAIN  346 566 HEMAGGLUTININ HAZ CHAIN.  FT CARBOHYD  24 24 N-LINKED (GLCNAC) (POTENTIAL).  FT CARBOHYD  54 54 N-LINKED (GLCNAC) (POTENTIAL).  FT CARBOHYD  57 97 N-LINKED (GLCNAC) (POTENTIAL).  FT CARBOHYD  58 N-LINKED (GLCNAC) (POTENTIAL).  FT CARBOHYD  59 N-LINKED (GLCNAC) (POTENTIAL).  FT CARBOHYD  50 SEQUENCE  566 AA; 63530 MW; E70F87F0AE1178F4 CRC64;
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Q9e312	Q9q013	Q9q014	099104	Q9q015	Q9e7p5	09d103	Q9e7p6	09d104	Q9d130	Q9d105	Q9d127	Q9d121	Q9d120	P87685	Q9d124	P87689	09d106	Q9d126	Q9d129	Q9d122	Q9d125	Q9qkd1	Q9qkd2	Q9qkd3	Q84174	Q82517	Q82513	Q67053
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# ALIGNMENTS

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Query Match Best Local Similarity 100.0%; Pred. No. 2.2e-10; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	(HAI AND HAZ) LINKED BY A DISULFIDE BOND (BY SIMILARITY).  -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  EMBL; AJ289703; CAC18525.1;  HSSP; P03437; ZVIU.  InterPro; IPR001364; Hemagglutn. Pfam; PF00509; Hemagglutnin; 1. Pfam; PF00509; Hemagglutnin; 1. PRINTS; PR00329; HEMAGGLUTNIZ. PRODOM; PD0000225; HEMAGGLUTNIZ. PRODOM; PD000025; HEMAGGLUTNIZ. PRODOM; PD000025; HEMAGGLUTNIZ. STONAL  1 16 POTENTIAL.  SEQUENCE 566 AA; 63356 MW; OBA681329300F72F CRC64;	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  STRAIN-CLONE 7A (H3N2);  MORSIN M.A., MOTTIS S.J., Smith H., Sweet C.;  MORSIN M.A., MOTTIS S.J., Smith H., Sweet C.;  "Influenza virus-induced apoptosis: a dual role for viral neuraminidase.";  "Influenza virus-induced apoptosis: a dual role for viral neuraminidase.";  Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.  -I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).	Ol-MAR-2001 (TrembLrel. 16, Created) Ol-MAR-2001 (TrembLrel. 16, Last sequence update) Ol-MAR-2001 (TrembLrel. 19, Last annotation update) HAEMAGGLUTININ PRECURSOR. Influenza A virus H3N2. Viruses; ssrNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses A virus. NCBL_TaxID-41857;	ILT 1 IGO Q9DHGO PRELIMINARY; PRT; 566 AA.

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RESULT OF RESULT
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067126;
01-NOV-1996 (TIEMBLIEL (
01-NOV-1996 (TIEMBLIEL (
01-DEC-2001 (TIEMBLIEL )
                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses. NCBI_TaxID-11320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interero; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutlnin; 1.
PRINTS; PR00329; HemAGGLUTIN; 1.
PRODOm; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein; Hemagglutlnin.
SEQUENCE 566 AA; 63456 MW; AE556302A9EEB99F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Callan R.J., Early G., Kida H., Hinshaw V.S.;
"The appearance of H3 influenza viruses in seals.";
J. Gen. Virol. 76:199-203(1995).
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).
-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAI
(HAI AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                      STRAIN=A/SEAL/MA/3984/92;
MEDLINE=95146951; PubMed=7844533;
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MEDLINE=95146951; PubMed=7844533;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             Influenza A virus.
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allan R.J., Early G., Kida H., Hinshaw V.S.;
The appearance of H3 influenza viruses in seals.";
The appearance of H3 influenza viruses in seals.";
Gen. Virol. 76:199-203(1995).
I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

CELL RECEPTORS AND FOR THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HAZ) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
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Pred. No. 2
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Best Local S
Matches 23
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Best Local Similarity
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Q67132;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                                                                                                                                                                              InterPro; IPR001364; Hemagglutn.
InterPro; IPR001364; Hemagglutinin; 1.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTNI2.
ProDom; PD000225; Hemagglutn; 1.
ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein; Hemagglutinin.
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HEMAGGLUTININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (In) Carlile M.J., Collins J.F., Moseley B.E. B. (eds.);
SYMPOSIUM OF THE SOCIETY FOR GENERAL MICROBIOLOGY, pp.285-311,
Cambridge University Press, New York (1981).
-1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).
-1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
(HALLAND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Influenza A virus (strain A/Aichi/2/68).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influ
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M55059; AAA43239.1; HSSP; P03437; 1HGE.
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Fiers W.;
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  346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Shift and drift in influenza viruses.";
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                                          2 GLFGAIAGFIENGWEGMIDGWYG 24
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                                                                                            Conservative
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63441 MW;
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100.0%; PI
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                                                                                       Score 134; DB; Pred. No. 2.2

O; Mismatches
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Pred. No.
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2.2e-10;
                                                                                                                2.2e-
                                                                                                                                         DB 12;
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Q91MA7;
Q1-DEC-2001
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Both G.W., Sleigh M.J.;

Both G.W., Sleigh M.J.;

"Conservation and variation in the hemagglutinins of Hong Kong;

"Conservation and variation in the hemagglutinins of Hong Kong;

"Conservation and variation in the hemagglutinins of Hong Kong;

"Conservation and variation in the hemagglutinins of Hong Kong;

J. Virol. 39:845-853(1991).

J. Virol. 39:845-853(1991).

J. Virol. 39:845-853(1991).

T. TORDERORS AND FOR INITIATING INFECTION (BY SIMILARITY)
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01-DEC-2001
                                                                                                                                                     Viruses; ssRNA negative-strand influenza virus A and B group; NCBI_TaxID=108859;
                                                            SEQUENCE FROM N.A.
STRAIN-A/HONG KONG/1/68(H3N2);
                                                                                                                                                                                                                                                                                               HEMAGGLUTININ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00329; HEMAGGLUTN12.
Probom; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein; Hemagglutinin;
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-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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T. Virol. 37:845-853(1981).
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Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.;
"Antigenic drift in the hemagglutinin of the Hong Kong influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-81053698; PubMed-6253883
Both G.W., Sleigh M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae, Influenza virus A and B group; Influenza A viruses.
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01-DEC-2001 (TrEMBLrel.
HEMAGGLUTININ PRECURSOR
                              MEDLINE-21287244; PubMed-11371620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                       Influenza A virus (A/Hong Kong/1/68(H3N2))
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   .G., Liu H.,
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01-MAR-2001
01-DEC-2001
STRAIN-A/SHOREBIRD/TAIWAN/31-4/99;
Lee M.S., Cheng P.C., Shien J.H., Cheng M.C., Lee L.H.,
"Identification and subtyping of avian influenza virus
transcription-polymerase chain reaction.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q910M5;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                Viruses; ssRNA negative-strand Influenza virus A and B group; NCBI_TaxID=140665;
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01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
HEMAGGLUTININ (FRAGMENT)
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MEDIINE-21287244; PubMed-113/1020;
Brown E.G., Liu H., Kit L.C., Baird S., Nesrallah M.;
Pattern of mutation in the genome of influenza A virus c

*Pattern of mutation in the mouse lung: Identification
                                                               SEQUENCE FROM N.A.
                                                                                                                    Influenza A virus (A/Shorebird/Taiwan/31-4/99).
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EMBL;
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NCBI_TaxID-108859;
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STRAIN-A/PHILIPPINES/2/82/BS (H3N2);
Hartley C.A., Ward A.C., Anders E.M.;
Hartley C.A., Ward A.C., Anders E.M.;
"Virulence of influenza virus for mice is associated with loss of oligosaccharide from the hemagglutinin molecule.";
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INPECTION (BY SIMILARITY).

-I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HAZ) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
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-i- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAI (HAI AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
EMBL; AF311750; AAC33016.1; -.
InterPro: IPR001364; Hemagglutn.
PRINTS; PR00329; HEMAGGLUTN12.
PRINTS; PR00329; HEMAGGLUTN11.
PRINTS; PR00329; Hemagglutn; 1.
Envelope protein; Glycoprotein; Hemagglutnin.
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SEQUENCE 301 AA; 32701 MW; 62A403758B764D57 CRC64;
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Envelope protein; Glycoprotein;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat-
HEMAGGLUTININS HAI AND HAZ (FRAGMENT).
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NCBI_TaxID=11320;
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Pred. No.
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  PRT;
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                                                                                                                                                                                                                                                                                                                                                   50BD62B6BFE11FD8 CRC64;
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Q82498;
01-NOV-1996
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01-NOV-1996 (
01-DEC-2001 (
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InterPro; IPRO01364; Hemagglutn.
                                          STRAIN-A/PHILIPPINES/2/82 (H3N2);
Hartley C.A., Ward A.C., Anders E.M.;
"Virulence of influenza virus for mice
oligosaccharide from the hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                         Viruses; ssRNA negative-strand Influenza virus A and B group;
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ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein;
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-I- SIMILARITY: BELONGS TO THE INFLUENZA HEMACOTIME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Changes in the hemagglutinin molecule of influenza type virus associated with increased virulence for mice."; Arch. Virol. 142:75-88(1997).
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STRAIN=A/PHILIPPINES/2/82 (H3N2);
                                    Submitted
                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA negative-strand unclassified Orthomyxoviridae.
            SEQUENCE FROM N.A
                                                                                                                NCBI_TaxID-11320;
                                                                                                                                                  Influenza A virus.
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MEDLINE-97300854; PubMed-9155874;
Hartley C.A., Reading P.C., Ward J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Influenza virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Virulence of influenza A virus for mouse lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ward A.C.;
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61745 MW;
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Pred. No. 4e-10;
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Influenza
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Best Local
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                                                                                                                      InterPro; IPR001364; Hemagglutn. Pfam; PR00509; Hemagglutinin; 1. Pfam; PR00509; HEMAGGLUTW12. PRODOM; PD000225; Hemagglutn; 1. Envelope protein; Glycoprotein; He SEQUENCE 566 AA; 63362 MW; 1FB
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Nakajima S., Takeuchi Y., Nakajima K.;

"Location on the evolutionary tree of influenza H3 haemagglutinin genes of Japanese strains isolated during the 1985-6 season.";

Epidemiol. Infect. 100:301-310(1988).

-i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

-i- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HA1 AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

EMBL; U08858; AAA18781.1; -.

EMBL; U08858; P03437; 2VIU.

InterPro; IPR001364; Hemaggluttn.

Pfam; PF00509; Hemaggluttnin; 1.
                                                                                                                                                                                                                                                                                                                                                                                     "Recent H3N2 swine influenza virus with haemagglutinin and nucleoprotein genes similar to 1975 human strains.";
J. Gen. Virol. 76:697-703(1995)
-- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).
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01-NOV-1996
01-NOV-1996
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                             CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

-I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA negative-strand viruses; Influenza virus A and B group; Influenza NCBI_TaxID=11320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elazhary Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bikour M.H.,
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MEDLINE=95205091; PubMed=7897358;
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PRINTS; PR00329; HEMAGGLUTN12.
ProDom: PD000225; Hemagglutt; 1.
Envelope protein; Glycoprotein; Hemagglutinin.
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Nakajima S., Takeuchi Y., Nakajim
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    "cloning and dna sequence of double-stranded copies of haemagglutinin genes from h2 and h3 strains elucidates antigenic shift and drift in human influenza virus.";
Nature 287:301-306(1980).
  Nature
[2]
                                                                                              STRAIN-A/FUKUOKA/C29/85 (H3N2);
MEDLINE-81030852; PubMed-7421990;
Gething M.-J., Bye J., Skehel J.,
                                                                                                                                                                                                                                                                                                                 Q67050;
01-NOV-1996 (TrEMBLrel.
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NCBI_TaxID=11320;
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Submitted (XXX-1991)
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                                                                                                                                                           SEQUENCE FROM N.A.
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Pfam; PF00509; Hemagglutinin; 1.
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1: FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
EMBL; M65018; AAA43151 1...
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                                                                                                                             SEQUENCE FROM N.A.

REDILINE-93233219; PubMed-7682624;

RX MEDLINE-93233219; PubMed-7682624;

RA Okuno Y., Isegawa Y., Sasao F., Ueda S.;

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Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
Envelope Protein; Glycoprotein; Hemagglutinin.
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SICHUAN/2/87 (H3N2);
MEDLINE-81030852; PubMed-7421990;
MEDLINE-81030852; PubMed-7421990;
Gething M.J. Bye J., Skehel J., Waterfield M.;
"Cloning and dna sequence of double-stranded copies of haemagglutinin genes from h2 and h3 strains elucidates antigenic shift and drift in human influenza virus.";
Nature 287:301-306(1980).
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067051; O1-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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Okuno Y. Isegawa Y. Sasao F., Ueda S.;

"A common neutralizing epitope conserved between the hemagglutinins of influenza a virus H1 and H2 strains.";

J. Virol. 67:2552-2558(1993).

-i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

-i- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
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     PRINTS;
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STRAIN-A/FUKUOKA/C29/85 (H3N2);
                                    r.terPro; IPRO01364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
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                                                                                     ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein;
NON_TER 1 1
NON_TER 109 109
SEQUENCE 109 AA; 12293 MW; 1
 40
         2 GLFGAIAGFIENGWEGMIDGWYG
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GIFGAIAGFIENGWEGMVDGWYG
                                               Similarity
                                      Conservative
                                              91.6%;
                                     ?;
62
                                              Score 131; DB 12;
Pred. No. 8.9e-11;
                  24
                                                                                       17EC66752DB8672F
                                      Mismatches
                                                                                                                   Hemagglutinin.
                                      0
                                                                                       CRC64;
                                                       Length 109;
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Search completed: July 1, 2002, 06:30:58 Job time: 690 sec

OM protein – protein search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Result
No.
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Listing first 45 summaries
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                                                                                                                                                                                                                                                  Score
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Gapop 10.0 ,
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AAR26004
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AAE04955	AAW75448	45	7	7	AAE04951	4	AAW01669	9	AAP70710	840	AAY70057	20	AAW44946	0494	AAP70711	AAP40615	AAR60194		AAR60221			88		26	35	9	403	S.	808	36	ABB02537	B010	AAY89680	
luenza virus	luenza virus	luenza		A/Shar		virus	Influenza A/Beijin	e hemagglut	ne influenza	S	d-adapted equi		Fontaineblea	መ	quine influenza	~	nic	uence o	מ	a haemaq	of the	of the	uenza virus a	fied clo	length H3N	req	sequence	ro -	polype	P178-like/bP10	l core polype	al DP178/107	Core polypeptide f	

# ALIGNMENTS

AAB13782 HA peptide; cytostatic; vaccine; cytotoxic T cell; CTL; immunotherapy; major histocompatibility complex class 1; MHC class 1; antigen; tumour; prostate; breast; multiple myeloma. AAB13782 standard; peptide; 24 AA. (DEND-) DENDREON CORP. 14-DEC-1998; 14-DEC-1999; 22-JUN-2000 WO200035949-A1 Unidentified Soluble peptide antigen HA 10-NOV-2000 AAB13782; (first entry) 98US-0112324. 99WO-US29724

Antigens modified by the covalent addition of a peptide that facilitates entry into antigen presenting cells, useful for producing compositions for immunizing against tumors and pathogens -  $\frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \int_$ 

WPI; 2000-442365/38.

Laus

Hakim I, Vidovic

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Best Local
                                           The sequences given in AARZ6004-19 are influenza fusion peptides, derived from the influenza virus haemaggiuthinin gene which were used for the preparation of synthetic membrane vessicles. The arrangment of at least one, pref. three cystein residues at one end of these peptides has been found useful for the fusion activity, for the fusion of the liposome to the target cell membrane. The liposomes produced using these peptides can contain at least one active drug and can be used to target cells infected with cancer
                                                                                                                                                                                                                                          Drug-contg. phospholipid bi:layer vesicle with cell-specific markers on membrane - where markers have at least 90 per cent biological activity, used as pharmaceuticals against e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to compositions of modified soluble protein antigens capable of eliciting an enhanced in vivo cyrotoxic T cell (CTL) response i.e. a major histocompatability complex (MHC) class I molecule response. The protein antigen is modified by the covalent addition of a peptide sequence which facilitate entry of the antigen into antigen presenting cells (APCs). The present sequence is one such peptide sequence which can be used to modify the soluble antigens. The present sequence is peptide HA. The modified antigen composition may be used for immunising against, or treating a tumour e.g. prostate and breast carcinoma or multiple myeloma, or pathogen in mammals.
                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                  WPI; 1992-270078/33
                                                                                                                                                                                                                                                                                                                                                   Gluck R,
                                                                                                                                                                                                                                                                                                                                                                                                                   02-FEB-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Influenza fusion peptide #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR26004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR26004 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemagglutinin; cystein; liposome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2;
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                                                                                                                                                                                               Fig 2; 13pp; English
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A
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                                                                                                                                                                                                                                                                                                                                                   Klein P;
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Pred. No. 1.2e-14;
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Sequence

26

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Query Match Best Local : Matches

Similarity

100.0%; St 100.0%; P7

Score 143; DB 18; Pred. No. 1.4e-14;

Length Indels

26;

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Gaps

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Mismatches

Conservative

Sequence

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RESULT
AAW34269
ID AAW3
XX AAW3
XX AAW3
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XX YITC
XX VITC
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                                                                             cc peptides are used as drug delivery systems, preferably for connections of the work of genetic material to target cells or tissues, cc particularly for diagnosis, treatment (especially antisense treatment) cc particularly for diagnosis, treatment (especially antisense treatment) contained to concern leukaemia and viral infections in humans or animals. Genetic material is delivered, without infection, to resting or proliferating cc cells, in vitro or in vivo. When the genetic material is an antisense cc cells, in vitro or in vivo. When the genetic molecule, it is targeted to mRNA encoding a (proto)oncogene. The cc continuous lipid layer does not leak. The peptides do not need to fuse continuous lipid layer does not leak. The peptides do not need to fuse cc with, or destabilise, plasma membranes in order to enter the cytoplasm, cc since the fusion peptide ensures cell penetration by endocytosis (after which fusion of the vesicle and endosomal membrane occurs). The genetic material thus has a greater chance of reaching the nucleus before it is degraded or expelled. Transfer of the material is 1000-20000 times more efficient than when using liposomes or conventional virosomes, so cannet conventional virosomes, so conventional virosomes, so convention to the convention of the west of the material is 1000-20000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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                                                                smaller doses can
genetic material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polycationic lipid and at least one natural or synthetic viral fusion peptide integrated in, or covalently linked to, the membrane. Such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virosome; vesicle; cationic lipid bilayer; viral fusion peptide; drug delivery system; membrane; gene therapy; diagnosis; treatme cancer; leukaemia; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vesicle with cationic lipid bilayer that includes viral fusion peptide - used for delivery of genetic material to cells, espe for gene therapy of cancer, leukaemia and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glueck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            charged lipid bilayer membranes composed of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9741834-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides AAW34269-W34284 represent novel lipid vesicles with positively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NIKA-) NIKA HEALTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96EP-0107282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-EP02268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROD LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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Pred. No. 1.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the membrane. Such
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                                                                                           with the
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AAB13784
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AAB70090
                                                     RESULT
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                                                                                                                                          Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                        polypeptides. The cationic virosome is a lipid bilayer vesicle comprisis a membrane with a net positive charge and contains 5-30 weight & based total lipids, 1,3-dioleoyloxy-2-(6-carboxy-spermy)-propyl-amide (DOSPER), together with other lipids and at least one active fusogenic peptide. The fusogenic peptide is a viral haemagylutinin that causes the vesicle to be internalized by target cells through phagocytosis or endocytosis. The virosome is useful for delivering a desired drug or substance, preferably a nucleic acid, to target cells (resting or proliferating mammalian cells) such as cancer cells, leukaemic cells or virally infected cells in vitro, in diagnostic or medical applications and for the manufacture of medicament for carrying out non-infectious gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipid bilayer vesicle, useful for delivering drugs to target cells as cancer, leukemic, or virally infected cells, comprises viral glycoproteins in positively charged membrane.
   AAB13784;
                          AAB13784 standard; peptide; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cationic virosome; cytostatic; gene therapy; lipid bilayer vesicle; viral haemagglutinin; drug delivery; cancer; leukaemia; viral infection; crosslinker.
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a crosslinker which is capable of linking surface of a novel cationic virosome and is capable of binding polypeptides. The cationic virosome is a lipid bilayer vesicle con
                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 14; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-233042/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NIKA-) NIKA HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-2000; 2000NZ-0332666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cationic virosome
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                                                                                                                1 CGLFGAIAGFIENGWEGMIDGWYG
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                                                                                                                                                                                                                                 therapy.
                                                                                                                                                       Similarity
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                                                                                                                                          100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                         Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crosslinker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROD LTD
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                                                                                                                                          Score 143; DB 22;
Pred. No. 1.4e-14;
; Mismatches 0;
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                                                                                                                                          Indels
                                                                                                                                                                Length 26;
                                                                                                                                                                                                                                                                                                                                                          vesicle comprising
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RESULT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                         Matches
                              Synthetic.
Influenza
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WO9730170-A1
                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigens modified by the covalent addition of a peptide that facilitates entry into antigen presenting cells, useful for compositions for immunizing against tumors and pathogens \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pk peptide; cytostatic; vaccine; cytotoxic T cell; CTL; immunotherapy;
major histocompatibility complex class 1; MHC class 1; antigen; tumour;
prostate; breast; multiple myeloma; HA peptide.
                                                                                            Membrane active;
                                                                                                                                                            02-MAR-1998
                                                                                                                                                                                              AAW29226;
                                                                                                                                                                                                                          AAW29226 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                          Membrane active acidic peptide INF6 from WO9730170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 26; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-442365/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DEND-) DENDREON CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                       1 CGLFGAIAGFIENGWEGMIDGWYG
                                                                                                                                                                                                                                                          6
                                                                           therapy;
                                                                                                                                                                                                                                                                                                        cglfgaiagfiengwegmidgwyg
                                                                                                                                                                                                                                                                                                                                                                       24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        44
                                                                                                                                                                                                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative 0,
                                                                                                                                                          (first entry)
                                                                          ve; acidic peptide; cationic lipid; transfection;
tumour; vaccine; cytokine gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US29724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0112324.
                                                                                                                                                                                                                          peptide; 23
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                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                     Score 143; DB 21;
Pred. No. 2.5e-14;
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                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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RESULT
AAR98016
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Best Local
28-SEP-1994;
                                                                                                                                                                                                                                                                                                                                           endosome membrane disruption promoting component; cationic polyamine; multifunctional molecular complex; foodstuff; herbicide; insecticide; plant growth regulator; miticide; rodenticide; fungicide; parasiticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preferably 0-2. The present sequence represents a specifically claimed acidic peptide for use in the composition. The composition is used for transfection in vitro, in vivo or ex vivo, particularly for gene therapy. A typical application is production of tumour vaccines from autologous cells transfected with a cytokine gene. The acidic peptide destabilises the endosomal membrane and significantly increases transfection efficiency, e.g. by as much as 1000 times, equivalent to that achieved with the optimal amount of cationic lipid. The acidic peptide also makes the transfection complex less sensitive to serum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A new composition has been developed for transfecting higher eukaryot cells contains: (1) a complex of nucleic acid to be expressed plus a suboptimal concentration of one or more cationic lipids, and optional at least one auxiliary lipid; and (ii) the new feature, at least one membrane-active, acidic peptide; where the ratio total positive charges:total negative charges in the composition is about 0-3,
                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition containing nucleic acid complexed with cationic lipid and a membrane-active, acidic peptide - used to increase efficiency of transfection by destabilising the endosomal membrane, especially
                                                                                                                  04-APR-1996
                                                                                                                                                                             WO9610038-A1
                                                                                                                                                                                                                                                                                             hyperproliferating
                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusogenic peptide; spike glycoprotein; enveloped virus; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR98016 standard;
                                                          .:3-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BOEH ) BOEHRINGER INGELHEIM INT GMBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for gene therapy
                                                                                                                                                                                                                                                                                                                            ide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide derived from HA-2 spike glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
                                                                                                                                                                                                                                                                                                                      immunisation; pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mechtler K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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94US-0314060
                                                          95WO-US12502
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                                                                                                                                                                                                                                                                                                disease
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Pred. No. 2.6e-13;
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                                                                                                                                                                                                                                                                                                                      therapy; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 23;
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AAR26005
ID AAR2
XX AAR2
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PR 02-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local :
                                           WPI; 1992-270078/33
                                                                                                                                       Gluck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR98010-R98041 represent fusogenic peptides derived from spike glycoproteins of enveloped viruses. These fusogenic peptides act endoscome membrane disruption promoting components (EMDPCs). These
                                                                                                                                                                                                                                                                                                                     02-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                             02-FEB-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemagglutinin; cystein; liposome
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                                                                                                                                                                                                                         (NIKA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza fusion peptide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR26005 standard; peptide;
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                                                                                                                                                                                                                              NIKA
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                                                                                                                                  Herrmann P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
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                                                                                                                                                                                                                              HEALTH PROD LTD
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100.0%;
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                                                                                                                                  Klein P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
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ches 0;
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RESULT
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Best Local .
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charged lipid bilayer membranes composed of a cationic and/or polycationic lipid and at least one natural or synthetic viral fusion peptide integrated in, or covalently linked to, the membrane. Such peptides are used as drug delivery systems, preferably for (non-)specific delivery of genetic material to target cells or tissues, particularly for diagnosis, treatment (especially antisense treatment) of cancer, leukaemia and viral infections in humans or animals. Genetic
                                                                                                                                                                Vesicle with cationic lipid bilayer that includes viral fusion peptide - used for delivery of genetic material to cells, espe for gene therapy of cancer, leukaemia and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAR26004-19 are influenza fusion peptides, derived from the influenza virus haemaggluttnin gene which were used for the preparation of synthetic membrane vessicles. The arrangment of at least one, pref. three cystein residues at one end of these peptides has been found useful for the fusion activity, for the fusion of the liposome to the target cell membrane. The liposomes produced using these peptides can contain at least one active drug and can be used to target cells infected with cancer
                                                                                                    Peptides AAW34269-W34284 represent novel lipid vesicles with positively
                                                                                                                                                                                                                                                                                                                                              04-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drug-contg. phospholipid bi:layer vesicle with cell-specilic markers on membrane - where markers have at least 90 per cent biological activity, used as pharmaceuticals against e.g. cancer and AIDS
                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                      Glueck R,
                                                                                                                                                                                                                                                                                  (NIKA-) NIKA HEALTH PROD LTD.
                                                                                                                                                                                                                                                                                                                 08-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virosome; vesicle; cadrug delivery system; cancer; leukaemia; vi
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                                                                                                                                                                                                                                                      Klein P,
                                                                                                                                    Page 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cationic lipid bilayer; viral fusion peptide;
em; membrane; gene therapy; diagnosis; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide;
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100.0%;
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                                                                                                                                                                                                                                                        Waelti ER;
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Pred No.
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Best Local S
Matches 23
The present sequence is a crosslinker which is capable of linking to the surface of a novel cationic virosome and is capable of binding polypeptides. The cationic virosome is a lipid bilayer vesicle comprising a membrane with a net positive charge and contains 5-30 weight 8 based on total lipids, 1,3-dioleoyloxy-2-(6-carboxy-spermyl)-propyl-amide (DOSPER), together with other lipids and at least one active fusogenic peptide. The fusogenic peptide is a viral haemagglutinin that causes the vesicle to be internalised by target cells through phagocytosis or substance, preferably a nucleic acid, to target cells (resting or proliferating mammalian cells) such as cancer cells, leukaemic cells or virally infected cells in vitro, in diagnostic or medical applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   material is delivered, without infection, to resting or proliferating cells, in vitro or in vivo. When the genetic material is an antisense molecule, it is targeted to mRNA encoding a (proto)oncogene. The continuous lipid layer does not leak. The peptides do not need to fuse with, or destabilise, plasma membranes in order to enter the cytoplasm, since the fusion peptide ensures cell penetration by endocytosis (after which fusion of the vesicle and endosomal membrane occurs). The genetic material thus has a greater chance of reaching the nucleus before it is degraded or expelled. Transfer of the material is 1000-20000 times more efficient than when using liposomes or conventional virosomes, so smaller doses can be used, avoiding possible toxicity associated with the genetic material.
                                                                                                                                                                                                                                                        Lipid bilayer vesicle, useful for delivering drugs to target cells as cancer, leukemic, or virally infected cells, comprises viral glycoproteins in positively charged membrane
                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                        Walti ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cationic virosome; cy
viral haemagglutinin;
                                                                                                                                                                                                                                                                                                                                                                                        (NIKA-) NIKA HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-2000; 2000NZ-0504444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 - NOV - 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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23; Conser
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                                                                                                                                                                                                                      Page 14; 41pp;
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                                                                                                                                                                                                                                                      positively charged membrane
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in; drug delivery; cancer;
                                                                                                                                                                                                                                                                                                                                                                                        PROD LTD
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leukaemia; viral infec
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SSSS
      AAR98010-R98041 represent fusogenic peptides derived from spike classifier of enveloped viruses. These fusogenic peptides act as classifier endosome membrane disruption promoting components (EMDPCs). These sequences were used in a transfer moiety which makes up part of the complex of the invention. The multifunctional complex is used for the transfer of a nucleic acid composition to a target cell, and comprises the nucleic acid composition and a current cell, and comprises the nucleic acid composition and a composition of the nucleic acid composition. There are several different cationic polyamines that can be used in the complex, one of which contains one of these sequences linked via a bridging group to the main contains one of these sequences linked via a bridging group to the main contains one of these sequences linked via a bridging group to the main contains one of these sequences linked via a bridging growth contains one of these sequences linked via a bridging growth contains one of these sequences linked via a bridging growth contains one of these sequences linked via a bridging growth contains one of these sequences linked via a bridging growth contains one of these sequences linked via a bridging growth contains one of these sequences linked via a bridging growth contains one of the cationic polyamine. The products can be used for delivering contains one of the contains one and composition of the contains one of the main contains one of the contains one of the main contains one of the contains one of the main contains one of the contains one of the main conta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pusogenic peptide; spike glycoprotein; enveloped virus; vaccine; EMDPC, endosome membrane disruption promoting component; cationic polyamine; multifunctional molecular complex; foodstuff; herbicide; insecticide; plant growth regulator; milicide; rodenticide; fungicide; parasiticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane disruption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New complexes for nucleic acid transfer to target cells - comprising a nucleic acid compsn. and a cationic poly:amine with an endosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-200887/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boutin
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23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 30; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunisation; pathogen; therapy;
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Pred. No.
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                                                                 The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (9p41) protein sequences, especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any core polypeptide that may be introduced into a living system and that can function as a pharmacoligically useful peptide for the treatment or prevention of a disease. The core polypeptides are bloactive peptides selected from a growth factor, cytokine, differentiation factor, interleukin, interferon, colony stimulating factor, hormone or angiogenic factor. The peptides of the invention can be used for anti-fusogenic factor. The peptides of the invention can be used for anti-fusogenic treatments. Sequences AAX88651-Y90055 represent core polypeptide fragments that can be used in the invention. Some sequences and form hybrid polymerides
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Matches 23
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprises enhancer sequence
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100.0%; P
tive 0;
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3.3e-13;
thes 0;
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Query Match Best Local Similarity

93.7%; 100.0%;

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                                                                                                                         Query Match
Best Local
                                                                                                  Matches
                                                                                                                                                                                                                                                                           The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other acidor with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in
                                                                                                                                                                                                                    Sequence
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Matches 23
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                                         Anti-retroviral; DP178-like; DP107-like; antifusogenic; antiviral; HIV transmissic
                                                                                                          DP178-like/DP107-like
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                                                                                                                                                                                                    AAU13634;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in
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                                                            transmembrane protein gp41;
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                                                                                                                                                                                                                                                                                         The present invention relates to peptides which exhibit anti-retroviral CC activity. The peptides of the invention (AAUJ2559-AAUJ4009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds CC to amino acids 639-673 of the transmembrane protein gp41 from human CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention CC also relates to a method of identifying compounds that inhibit the CC formation of or disrupts a DP107/DP178 complex. The method comprises CC detecting the formation of a DP107/DP178 complex, both in the presence CC or absence of a test compound, in a reaction mixture containing DP107 cand DP178 peptides. The method is useful for identifying compounds, CC including small molecule compounds, which may themselves exhibit CC antifusogenic, antiviral or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human CC retroviral, particularly HIV, transmission to uninfected cells. The CC of the invention.
                                                                                                                                                               Query Match 93.7%; Score 134; DB 22; Best Local Similarity 100.0%; Pred. No. 3.6e-13; Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a DP107/DP178 complex -
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                                                                                                                                                                                                                                                            Sequence
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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### ALIGNMENTS

#### A; Molecule type: DNA A; Residues: 1-517 <DNA A; Cross-references: EMBL:AL353032; GSPDB:GN00061; ATSP:T20N10.250 A; Experimental source: cultivar Columbia; BAC clone T20N10 C; Genetics: hypothetical protein T20N10.250 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 08-Dec-2000 C:Accession: T49173 R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; C;Species: Parechinus angulosus (angulate urchin) C;Species: Parechinus angulosus (angulate urchin) C;Date: 31-Mar-1980 #sequence\_revision 31-Mar-1980 #text\_change 16-Feb-1997 C;Accession: A91090; A91091; A02586 R;Strickland, W.N.; Strickland, M.; de Groot, P.C.; von Holt, C.; Wittmann-Liebold, B. Eur. J. Blochem. 104, 559-566, 1980 A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus rminal cyanogen bromide peptides. A;Reference number: A91090; MUID:80156831 A;Contents: sequence of residues 1-84 A;Accession: A91090 submitted to the Protein Sequence Database, April 2000 A;Reference number: Z25017 A;Accession: T49173 A;Status: preliminary DЬ Ş A; Molecule type: protein A; Residues: 80-248 <ST2> A; Note: 144-Arg was also found C; Superfamily: histone H1 C; Keywords: DNA binding; nucleosome; sperm R;Strickland, W.N.; Strickland, M.; Brandt, W.F.; von Holt, C.; Lehmann, A.; Wittmann Eur. J. Biochem. 104, 567-578, 1980 A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus A;Reference number: A91091; MUID:80156832 A;Accession: A91091 A; Molecule type: protein A; Residues: 1-248 <STR> HSUR1P RESULT Query Match Best Local Similarity Matches 25; Conserv 146 KAAAKRKAALAKKKAAAKRKAAAKAKKAKKPKKKAAKKAKK 187 Conservative 49.38; 4; Score 103; DB 1; Length 248; Pred. No. 0.087; Mismatches 13; Indels C.; Lehmann, A.; Wittmann 0 Gaps Rudd, 0

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nucleoporin p62 homolog - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 05-Nov-1999
C:Accession: I52523
R:Wang, Z.O.; Akmal, K.M.; Kim, K.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zuotin-like protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Species: Schizosaccharomyces pombe
C:Accession: T39683; T40195
R:Oliver, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, March 1998
A; Reference number: Z21869
A; Reference number: Z21869
A; Accession: T39683
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                               Biol. Reprod. 51, 1022-1030, 1994
A;Title: An unusual nucleoporin related messenger ribonucleic A;Reference number: I52523; MUID:95151924
A;Accession: I52523
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Cross-references: GB:S75997; NID:g913245; PIDN:AAB33384.1; FA:Experimental source: testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Status: preliminary; translated from GB/EMBL/DDB. A; Molecule type: DNA
A:Rosidus: 39-442 <WOO>
A:Cross-references: EMBL:297992; PIDN:CAB10796.1; (A:Experimental source: strain 972h-; cosmid c30D10 C:Genetics: C:Genetics: SPDB:SPBC1778.01c; SPDB:SPBC30D10.01
A:Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Molecule type: DNA
A:Residues: 1-124 <CLI>
A:CROSS-references: EMBL:AL049489; PIDN:CAB39796.1; GSPDB:GN00067; SPDB:SPBC1778.01c
A:Experimental source: Strain 972h-; cosmid c1778
R:WOOD, V: Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, F. Submitted to the EMBL Data Library, February 1998
A:Reference number: Z21910
A:Accession: T40195
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A;Map position: 3
A;Introns: 312/3; 359/3; 444/3
C;Superfamily: Arabidopsis thaliana hypothetical protein F17J16.30
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Query Match
Best Local Similarity
                                                                                              Cross-references: GB:S75997; NID:g913245; PIDN:AAB33384.1; PID:g913246
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Best Local :
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Reprod. 51, 1022-1030, 1994
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  47.8%;
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56.0%;
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  Score 100;
Pred. No.
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Pred. No. 0
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DB 2;
0.13;
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zuotin - yeast (Saccharomyces cerevisiae)

N;Alternate names: probable Z-DNA-binding protein; protein G9554; protein YGR2
C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 21-Jul-2000
C;Accession: S25194; S64620; S19066
C;Zhoression: S25194; S64620; S19066
C;Zhoression: S25194; Herbert, A.; Winter, E.; Rich, A.
EMBO J. 11, 3787-3796, 1992
A;Title: Zuotin, a putative Z-DNA binding protein in Saccharomyces cerevisiae.
A;Reference number: S25194; MUID:93010971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S09388
R;Hill, C.S.; Martin, S.R.; Thomas, J.O.
EMBO J. 8, Z591-Z599, 1989
A;Title: A stable alpha-helical element in
A;Reference number: S09388; MUID:90060019
                                                                                                                                                                                       RESULT
S25194
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809388 histone H1 - sea urchin (Parechinus angulosus)
C:Species: Parechinus angulosus (angulate urchin)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: S09388
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C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
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A; Residues: 1-206 <HIL>
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A:Residues: 1-380 <AAA>
A:Cross-references: EMBL:AL137556
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R; Ottenwaelder, B.;
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Best Local Similarity
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100.0%; Pred. No. 0.
tive 0; Mismatches
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Pred. No. 0.19;
4; Mismatches
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A;Accession: S25194
A;Molecule type: DNA
A;Residues: 1-433 <ZHA>
A;Coss-references: EMBL:X63612; NID:g4836; PIDN:CAA45156.1; PID:g4837
A;Cross-references: EMBL:X63612; NID:g4836; PIDN:CAA45156.1; PID:g4837
A;Coss-references: EMBL:X63612; NID:g4836; PIDN:CAA45156.1; PID:g4837
A;Note: part of this sequence, including the amino end of the mature protein, was confision for the protein Sequence Database, May 1996
A;Reference number: S64611
A;Accession: S64620
A;Molecule type: DNA
A;Residues: 1-433 <VOE>
A;Cross-references: EMBL:Z73070; NID:g1323520; PID:e243256; PID:g1323521; MIPS:YGR285c
A;Experimental source: Strain S288C
C;Genetics:
nuclear protein SR-25 - mouse (Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000 C; Accession: JC7219
R; Sasahara, K.; Yamaoka, T.; Moritani, M.; Tanaka, M.; Iwahana, H.; Yoshimoto, Biochem. Biophys. Res. Commun. 269, 444-450, 2000
A; Title: Molecular cloning and expression analysis of a putative nuclear protein A; Recession: JC7219; MUID: 20175222
A; Accession: JC7219
A; Molecule type: mRNA A; Residues: 1-229 <SAS>
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A;Cross-references: SGD:S0003517; MIPS:YGR285c
A;Map position: 7R
C;Superfamily: dnaJ amino-terminal homology
C;Keywords: DNA binding; nucleus
F;97-168/Domain: dnaJ amino-terminal homology <DNJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, A
A:Reference number: Z18935
A:Accession: T18513
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A; Residues: 1-166 <LAW>
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T18513
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A; Note: C0845c
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Matches 23
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Best Local Similarity
Matches 19; Conserv
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82.6%;
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Pred.
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Pred. No. 0.45;
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0.27;
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                                                                           of a putative nuclear protein,
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A; Molecule type: DNA
A; Residues: 1-153 <FAB>
A; Cross-references: EMBL: U16726; NID: g571479; PIDN: AAA98454.1;
A; Note: the authors did not translate the codon for residue 1
C; Superfamily: histone H2B
                                                                                                                                                                                                                                       R;Fabry, S.; Mueller, K.; Lindauer, A.; Park, P.B.; Cornelius, T.; Schmitt, Curr. Genet. 28, 33-345, 1995
A;Title: The organization structure and regulatory elements of Chlamydomonas A;Reference number: S59581; MUID:96120862
A;Accession: S59591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: A86315
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: A86315
                                                                                                                                                                                                                                                                                                                                                      histone H2B (clone CH-IV) - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 23-Jul-1999
C;Accession: S59591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE005172; NID:g9665074; PIDN:AAF97276.1; GSPDB:GN00141 C;Genetics:
A;Map position: 1
                                                                                                                                                                                                           A:Status: preliminary; nucleic acid sequence
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A; Residues: 1-383 <STO>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
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A;Experimental source: MIN6 cell line
C;Comment: This protein is a highly hydrophilic nuclear protein with a serine-arginin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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Best Local S
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Best Local :
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43.18;
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Score 90;
Pred. No.
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Pred. No. 1.1;
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Pred. No. 0.7;
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                      DB 2;
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Local

25; Conserv

Conservative

Mismatches

16;

Indels

6,

Gaps

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RESULT 13
T50609
Typothetical protein DKFZp761B2423.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Cate: 21-Ju1-2000 #sequence_revision 21-Ju1-2000 #text_change 21-Ju1-2000
C;Cates 21-Ju1-2000 #sequence_revision 21-Ju1-2000 #text_change 21-Ju1-2000
C;Catession: T50609
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, June 2000
A;Reference number: Z25143
A;Accession: T50609
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Cates preliminary
A;Cross references: EMBL:AL359564
A;Cross references: EMBL:AL359564
A;Cross references: EMBL:AL359564
A;Cross references: adult amygdala; clone DKFZp761B2423
C;Genetics:
C;Genetics:
                                             RESULT 14
T23778
h1stone H1.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C:Accck.sion: T23778; T42231; S09130; S01817
R:Percy, C
submitted to the EMBL Data A; Reference number: 219798
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C:Species: Plasmodium falciparum
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Ju1-2000
C:Accession: F71619
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
A;Accession: F71619
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A;Experimental source: Clone 3D7
C;Genetics:
A;Gene: PFB0235w
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F71619
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17; Conserv
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45.0%; Pred. No.
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85.0%;
                      Library, August 1996
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Pred. No. 1.4;
3; Mismatches
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A;Residues: 1-208 (JED)
A;Cross-references: EMBL:AF017810; PIDN:AAB70665.1
A;Cross-references: EMBL:AF017810; PIDN:AAB70665.1
A;Sanicola, M.; Ward, S.; Childs, G.; Emmons, S.W.
J. Mol. Biol. 212, 259-268, 1990
A;Title: Identification of a Caenorhabditis elegans histone | A;Reference number: S09130; MUID:90204554
A;Accession: S09130
A;Crossion: S09130
                                                                                                                                                                                                                                                                cgcr-4 protein - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: S19113; S14466
R;Wakarchuk, W.W.; Mueller, F.W.; Beck, C.F.
Plant Mol. Biol. 18, 143-146, 1992
A;Title: TWO GC-rich DNA elements of Chlamydomonas reinhardtii with complex arrangem
A;Reference number: S19113; MUID:92119224
A;Accession: S19113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-43,'T',45-83,'H',85-100,'R',102-208 <SAN>
A;Residues: 1-43,'T',45-83,'H',85-100,'R',102-208 <SAN>
A;Cross-references: GB:X53277; NID:g10885; PIDN:CAA37372.1; PID:g10886
R;Vanfleteren, J.R; van Bun, S.M.; van Beeumen, J.J.
Blochem. J. 255, 647-652, 1988
A;Title: The primary structure of the major isoform (H1.1) of histone H1
A;Reference number: S01817; MUID:89076229
A;Accession: S01817
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A; Residues: 1-265 <W
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S19113
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                                                                                                                                                                      A;Cross-references: EMBL:X17208; NID:g18136; PIDN:CAA35080.1; PID:g18137
                                                                                                                                                                                                                                            A; Status: preliminary
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A; Introns: 79/3
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A; Residues: 2-43,'T',45-100,'K',102-208 <VAN>
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A; Accession: T42231
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A;Description: The histone H1 complement of Caenorhabditis elegans
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A; Residues: 1-208 <WIL>
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A;Status: translated from GB/EMBL/DDBJ
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Best Local Similarity
     Matches
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Pred. No.
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Pred. No. 0.93;
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Match
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Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
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209
                                                                                                                                                                                                                                                                                                                                                                                                                             105224 seqs, 38719550 residues
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  HI_PARAN
ZUOI_YEAST
HZBA_CHLRE
H11_CAEEL
TOLA_PSEAE
R112_METJA
H2B3_CHLRE
H12_VOLCA
PHPA_HACH
BRD3_HUMAN
RL12_PYRAB
YDJ3_YEAST
TOLA_ECOLI
HZB1_CHLRE
CBF5_ASPFU
NOP5_RAT
IF2P_YEAST
RL12_AERPE
H12_CHLRE
NOF5_YEAST
RL12_AERPE
H12_CHLRE
NOF5_YEAST
RL12_CHLRE
NOF5_YEAST
RL12_CHLRE
NOF5_YEAST
RL12_CHLRE
NOF5_YEAST
RL12_CHLRE
NOF5_YEAST
RLA1_TRYCR
H11_VOLCA
MST2_DROHY
H1_EUPEU
H11_CHICK
H11R_CHICK
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002752 plasmodium
010752 homo sapien
01085 pyrococcus
012117 saccharomyc
p19934 escherichia
p50565 chlamydomon
014007 schizosacch
057705 pyrococcus
043102 aspergillus
043102 aspergillus
049999 aeropyrum p
p40278 chironomus
044045 chlamydomon
012499 saccharomyc
090416 saccharomyc
000416 saccharomyc
p26643 trypanosoma
p2257 echinolampa
00864 volvox cart
008696 drosophila
p32103 euplotes eu
p06144 lytechinus
p08288 gallus gall
p15865 rattus norv
                                                                                                                                                                                                               P50600
P54048
                                                                                                                                                                                                                              P54347 chlamydomon
P10771 caenorhabdi
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                                                                                                                                                                                               chlamydomon volvox cart
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Query Matc Best Local Matches	15-JUL-19 21-JUL-19 21-JUL-19 15-JUL-19 Histone H Histone H Parechinu Eukaryota Echinoide Echinoide Echinoide Exprechinu NCBI_TaxI [1] SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE MEDLINE-8 SETICKIAnn Wittmann- "The prim Parechinu protein a SEQUENCE MEDLINE-8 SEQUENCE SEQUENCE MEDLINE-8 S	SULT 1 PARAN PONNO	30000000000000000000000000000000000000
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ngth 248; Indels	nida nida nida nida olt N-te SCNBr CNBr		P10412 P43274 P44678 Q58105 Q581105 Q12114 Q12114 Q122706 P22684 P15864 P15864 P43277 P77951 Q00132
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RESULT 2
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RESULT
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-1- FUNCTION: Z-DNA BINDING PROTEIN. CCHROMOSOME ORGANIZATION.
-1- SUBCELLULAR LOCATION: Nuclear.
-1- SUBCELLULAR CONTAINS 1 J DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993
01-OCT-1993
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P32527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P08622; 1XBL.
SGD; S0003517; ZUO1.
InterPro; IPR001623; DnaJ_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X63612; CAA45156.1; -. EMBL; Z73070; CAA97317.1; -. PIR; S25194; S25194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Volckhert G., Voet M., Robben J.;
Volckhert G., Voet M., Robben J.;
"Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the right arm of chromosome VII from Saccharomyces cerevisiae carrying the MAL1 locus reveals 15 complete open reading frames, including ZUO1, BGL2 and BIO2 genes and an ABC transporter gene.";
                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
Chaperone; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                Chaperone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00226; DnaJ; 1. SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=S288C / FY1679;
MEDLINE=97245295; PubMed=9090054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uniang S., Lockshin C., Herbert A., Winter "Zuotin, a putative Z-DNA binding protein cerevisiae.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93010971; PubMed-1396572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE STRAIN=20B-12;
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                                                                                                     Similarity
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433 AA;
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, 0AA76BC11D3C7DAB CRC64;
                                                                                                                                                                                                Score 96; DB 1
Pred. No. 0.16;
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H2B4_CHLRE
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DT 01-OCT
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DE Histon
OS Chlamy
OC Eukary
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Best Local
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InterPro; IPR000558; H.1stone_H2B.
InterPro; IPR000166; H.1stone_core.
Pfam; PF00125; h1stone; 1.
PRINTS; PR00621; HISTONEH2B.
PRODOM; PD000497; H1STONEH2B. 1.
SMART; SM00427; H2B; 1.
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=90204554; PubMed=1969492;

MEDLINE=90204554; PubMed=1969492;

Sanicola M., Ward S., Childs G., Emmons S.W.;

Sanicola M., Ward S., Childs G., Emmons B.W.;

"Identification of a Caenorhabditis elegans histone H1 gene family.

"Identification of a Caenorhabditis elegans histone H1 gene family.

"Identification of a Caenorhabditis elegans histone H1 gene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _CAEEL
                                                                                                                                                                                                                                                                                                                                                                                   H11_CAEEL
P10771;
01-JUL-1989
01-AUG-1991
15-JUL-1999
                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        HIS-24.
                                                                                                                                                                                                                                                                                                                                                            Histone H1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chromosomal protein; Nucleosome Multigene family. SEQUENCE 153 AA; 16587 MW; F
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophycuae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P54347;
01-OCT-1996
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Fabry S., Mueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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30-MAY-2000
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SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATELY 14 SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE HISTONE H2B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organization structure and regulatory elements of Chlamydomonas one genes reveal features linking plant and animal genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 43.18;
Similarity 51.08;
25; Conservative
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1 (Rel. 19,
9 (Rel. 38,
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                                                                                                                                                                                                                                                             Peloderinae;
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Hocleosome core; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=8590479;
K., Lindauer A.,
                                                                                                                                                                                                                                                             Nematoda; Chromadorea; Rhabditida; Rhabditoidea; cinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 90; DB Pred. No. 0.2; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Park P.B.,
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9.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cornelius
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding;
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RESULT
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Best Local S
Matches 23
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P50600;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                             PSEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89076229; PubMed=3202838; Van Beeumen Vanfleteren J.R., van Bun S.M., van Beeumen "The primary structure of the major isoform the nematode Caenorhabditis elegans."; Biochem. J. 255:647-652(1988).
                                                                                                                                                                                Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                Tola protein.
Tola OR PA0971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S09130; S09130.

PIR; S01817; S01817.

HSSP; P02259; 1HST.

InterPro; IPR001186; Linker_histone.

InterPro; IPR003216; Linker_histone; 1.

Pfam; PF00538; Linker_histone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentitles requires a license agreement (See http://www.isb-siborsend an email to license@isb-sib.ch).
                                           Dennis
                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 16-OCT-2001)
                     Dennis J.J., Lafontaine E.R., Sokol Facinity and Characterization
                                                            MEDLINE-97113525; PubMed-8955385
                                                                                                                                             NCBI_TaxID=287;
                                                                                                                                                                     Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                        SEQUENCE FROM N.A
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SUBCELLULAR LOCATION: Nuclear.
MISCELLANEOUS: THERE ARE 2 FORMS OF H1 IN THIS NEMATODE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X53277; CAA37372.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 53.5
23; Conservative
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ol. 212:259-268(1990)
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Last
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GLOBULAR.
H -> L (IN RFF
                                                                                                                                                                                      gamma
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                                                                                                                                                                                                                                                                       sequence update)
annotation updat
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Pred. No. 0.31
4; Mismatches
                                         Sokol P.A.;
                                                                                                                                                                                                                                                                                                                                                         PRT;
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-> K (IN REF. 2).
7802EA9AA4F36F6F CRC64;
                                                                                                                                                                                      subdivision;
                     o
f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1
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                     the tolQRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                      Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 207
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                   genes
                   of
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Best Local S
Matches 22
                                                                                                                                                                                                                                 LMETJA
RL12_METJA
                                                                                                                                                                                 01-OCT-1996
01-OCT-1996
16-OCT-2001
SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayn

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."; Nature 406:959-964 (2000).

-1- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                           50S ribosomal pro
                                                                                                          NCBI_TaxID=2190;
                                                                                                                        Methanococcus
                                                                                                                                Methanococcus jannaschii.
Archaea; Euryarchaeota; N
                                                                                                                                                                                                                        P54048;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
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STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; Pubmed-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transport;
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                                                                                                                                                                                                                                                                                                  124
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                                                                                                                                                                                                                                                                                                                                                              Similarity
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347 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                    Rel. 34, Last sequence update)
Rel. 40, Last annotation update)
protein L12P.
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34,
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37
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37935
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                                                                                                                              Methanococcales; Methanococcaceae;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PERIPLASMIC
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   Glodek A.,
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                           J.D.,
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01-OCT-1996 (Rel. 3
01-OCT-1996 (Rel. 3
30-MAY-2000 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-96120862; PubMed-8590479;

MEDLINE-96120862; PubMed-8590479;

Mueller K., Lindauer A., Park P.B., Cornelius Schmitt R.;

"The organization structure and regulatory elements of "The organization structure" and "The organizati
                                                                                                                         between the SW155 include. The European Bioinformatics Institute. The table by non-profit institutions as long use by non-profit institutions as long table.
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-I: FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS INVOLUED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR ACCURATE TRANSLATION (BY SIMILARITY).
-I: SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hust Hanna B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                          or send an
                                                                                                                                                                                                                                                                                                                                                            histone genes reveal features linking plant and animour. Genet. 28:333-345(1995).
-i- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \label{eq:charge_constraint} \textbf{Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.}
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Chlamydomonas reinhardtii.
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Ribosomal protein; Complete proteome.
SEQUENCE 102 AA; 10363 MW; 35306FFDE967C52C
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                        EMBL; U16725; AAA98450.1; -
                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                     and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
IPR000558;
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34, Last sequence
39, Last annotation
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52.6%;
Histone_H2B
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RESULT 8
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Best Local S
Matches 24
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pfam; Pr00125; histone; 1:
PRINTS; PR00621; HISTONEH2B.
ProDom: PD000497; Histone_H2B: 1.
SMART; SM00427; H2B; 1.
PROSITE; PS00357; HISTONE_H2B; 1.
Chromosomal protein; Nucleosome core
Multigene family.
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Q08865;
                              DOMAIN
DNA_BIND
DNA_BIND
DNA_BIND
         DOMAIN
REPEAT
                                                                           Repeat.
INIT_MET
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01-FEB-1995 (Rel. 31, Last seg
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                               EMBL; L07947; AAA34246.1;
PIR; JN0748; JN0748.
HSSP; P08287; 1GHC.
                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                        "Two histone H1-encoding genes of the green alga Volvox features intermediate between plant and animal genes."; Gene 129:59-68(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                          ProDom; PD000373;
SMART; SM00526; H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Histone H1-II.
                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Volvocaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Volvox carteri.
Eukaryota; Viridiplantae;
                                                                                               Chromosomal
                                                                                                                               Pfam; PF00538;
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93328125;
                                                                                                                                       InterPro; IPR001386; Linker_histone
InterPro; IPR003216; Linkerhist_N.
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                                                                                                                                                                                                                                                                                              NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
SUBCELLULAR LOCATION: Nuclear.
DEVELOPMENTAL STAGE: EXPRESSION IS RESTRICTED TO EMBRYOGENESIS.
SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                   FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
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24; Conservative
                                                                                                                   F00538; linker_histone; 1. PD000373; Linkerhist_N; 1.
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                                                                                               Nuclear
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annotation
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                               POTENTIAL.
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                                                                                              DNA-binding;
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                    P-K-K-A-[AK]-A.
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RESULT 9
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Best Local Similarity
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Q02752;
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                                                                                                                           Phosphorylation;
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                                                                                                                                         EMBL; M95789; AAA29732.1;
                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                          Plasmodium chabaudi.
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                                                                                                                                                                                                                                                                                                            MEDLINE=93116806; PubMed=1475002;
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.gen; Membrane; Rep.
OR 24 (POTENTAL).
ACIDIC PHOSPHOPROTEIN
16 X 8 AA TANDEM REPEATS.
1-1.
1-2.
209
1-3.
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1-4.
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1-5.
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1-6.
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1-7.
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1-8.
257
1-10.
1-11.
1-12.
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29,
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Pred. No. 0.71
7; Mismatches
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                                                                                                                        Membrane; Repeat; Erythrocyte
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kDa antigen).
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Best Local S
Matches 16
                                                                    EMBL; D26362;
EMBL; Z81330;
MIM; 601541;
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Q15059; Q92645;
16~OCT-2001 (Re
                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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CARBOHYD
CARBOHYD
SEQUENCE
      Ptam; PF00439; bromodomain; 2
PRINTS; PR00503; BROMODOMAIN.
SMART; SM00297; BROMO; 2.
PROSITE; PS00633; BROMODOMAIN
                                                                                                                                                                                                                    "Chromosomal localization, gene structure and it the ORFX gene, a homologue of the MHC-linked R. Gene 200:177-183(1997).
-i- SUBCELLULAR LOCATION: Nuclear (Potential).
-i- TISSUE SPECIFICITY: UBIQUITOUS.
-i- SIMILARITY: CONTAINS 2 BROMODOMAINS.
                                                                                                                                                                                                                                                                                                                                                         TISSUE-Bone marrow;
MEDLINE-96051398; PubMed-7584044;
Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., S
Seki N., Kawarabayashi Y., Ishikawa K.-I., Tabata S.;
"Prediction of the coding sequences of unidentified human
The coding sequences of 40 new genes (KIAA0041-KIAA0080) d
analysis of cDNA clones from human cell line KG-1.";
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REPEAT
                                                                                                                                                                                                                                                                                            SEQUENCE OF 363-726 FROM N.A. MEDLINE=98038990; PubMed=9373153; Thorpe K.L., Gorman P., Thomas C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                                                                                                Thorpe K.L., Gorman P., The "Chromosomal localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bromodomain-containing protein BRD3 OR RING3L OR KIAA0043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                        nterPro; IPR001487; Bromodomain
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                                                                                  CAB03630.1;
                                                                                             BAA05393.1;
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Pred. No. 1.4;
4; Mismatches
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-LINKED (GLCNAC. . .)
DB85E83E795EE7E5 CRC
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(RING3-like
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and transcription
ked RING3 gene.";
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PS50014;

BROMODOMAIN\_2;

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RESULT 11
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Q12117;
30-MAY-2000
30-MAY-2000
16-OCT-2001
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16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR ACCURATE TRANSLATION (BY SIMILARITY).
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DOMAIN
                                                                        YEAST
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16-OCT-2001 (Rel. 40,
50s ribosomal protein
RPL12P OR PAB1168.
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Pred. No. 0.54
2; Mismatches
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SER-RICH.
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Best Local :
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01-FEB-1991
16-OCT-2001
MEDLINE-90078104: PubMed-2687247;
Levengood S.K., Webster R.E.;
"Nucleotide sequences of the tola and tola their products, components of a multistep t
                                                                                                                                                                                                                                                                                                               TOLA_ECOLI
P19934;
                                                                                                                                                             Escherichia coli.
Bacteria; Proteobacteria;
Escherichia.
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TOLA OR CIM OR EXCC
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Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO THE ARCHAEAL OPSIN FAMILY. HSP30
                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
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EMBL; 268196; CAA92370.1;
SGD; S0002440; YDR033W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                            NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arnold W., Becker A.,
Submitted (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical 36.2\ kDa protein in RAD28-LYS14 intergenic region YDR033W OR YD9673.03.
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EMBL/GenBank/DDBJ
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J databases.
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Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Khura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                   Repeat; Inner
DOMAIN
                                                                                                                  EMBL; M28232; AAA24683.1;
EMBL; AE000177; AAC73833.1
EMBL; D90713; BAA35405.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lubkowski J., Hennecke F., Plueckthun A., Wlodawer "Filamentous phage infection: crystal structure of with its coreceptor, the C-terminal domain of Tola. Structure 7:711-722(1999).
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                                                     Transport;
                                                                     EcoGene;
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MEDLINE-99332679; PubMed-10404600;
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Derouiche R., Gavioli M., Benedet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTION WITH PORINS. MEDLINE-97133271; PubMed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yano M., Horiuchi T.; Yano M., Horiuchi T.; ^{\rm T}A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage m. DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gregor J., Davis N.W., Kirkpatrick H.A., Mau B., Shao Y.;
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burlan
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "TolA central domain interacts with Escherichia coli EMBO J. 15:6408-6415(1996).
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J. Bacteriol. 171:6600-6609(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A COLICINS (COLICINS A, E1, E2, E3, AND K). NECESSARY FOR THE COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION OF BACTERIOPHAGE DNA.
                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                                                                                                                                                                                                                                                                                                              AND LAMB
                                                                                                       JV0057;
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                                                                  EG11007; tolA.
Protein transport; Bacteriocir
ner membrane; 3D-structure; Con
13 CYTOPLASMIC
14 34 POTENTIAL.
                                                                                     20-MAY-99.
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AAC73833.1; -.
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ne protein involved
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                          Bacteriocin transport; Transmembrane; ructure; Complete proteome.
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/ed in colicin uptake
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                (POTENTIAL)
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Matches 23
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Matches 24
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01-OCT-1996
30-MAY-2000
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAIN
DOMAIN
                                                                                                                            PRINTS; PR00621; HISTONEH2B, ProDom; PD000497; Histone_H2B; SMART; SM00427; H2B; 1.
                                                                                                                                                           InterPro; IPR000558; Histone_H2B.
InterPro; IPR000166; Histone_core.
Pfam; PF00125; histone; 1.
                                                                                 SEQUENCE
                                                                                           Chromosomal prote
Multigene family
                                                                                                                PROSITE; PS00357; HISTONE_H2B; 1.
                                                                                                                                                                                                EMBL; L41841; AAA99967.1; -
                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                     structure."
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96017782; PubMed-7479007;
Walther Z., Hall J.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Chlorop Chlamydomonadaceae; Chlamydomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AAAAAEAAAAEAAA-----
                                                                                                                                                                                                                                                                                                                       Leic Acids Res. 23:3756-3763(1995)
SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING
H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATELY 14
SUBCELLULAR LOCATION: Nuclear:
Similarity
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                                                                                                    protein; Nucleosome core; Nuclear protein;
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    Last annotation updat

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DOMAIN II (ALPHA-HELICAL).

DOMAIN III (FUNCTIONAL).

10 x TANDEM REPEATS OF (ED).

A(2,4).
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Pred.
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Pred. No.
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                        Mismatches
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                                   NO 2;
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                       16;
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                                             Length 153
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                       Indels
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Best Local Similarity
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014007;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Centromere/microtubule binding protein cbf5 (Centromere-binding factor 5) (Nucleolar protein cbf5).
CBF5 OR SPAC29A4.04C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetaee;
Schizosaccharomyces.
Schizosaccharomyces.
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Brown D., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;

Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: BINDS IN VITRO TO CENTROWERES AND MICROPUBULES, IT IS A CENTROMERE DAA. CBF3 BEINDIM FACTOR AND IS INVOLVED IN MITOTIC CHROMOSOME SEGREGATION. IT IS ESSENTIAL FOR CELL GROWTH (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).

-I- SIMILARITY: BELLONGS TO THE TRUB FAMILY OF PSEUDOURIDINE SYNTHASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                  440 EAAKKEEKRRKKE----AKKEKKEKKEKKEKKKKK 472
                                                                                 466
474 AA;
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450
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                                                                                                                                                                                           468 7
53110 MW;
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456
459
462
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             2002, 06:31:35
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7 X 3 AA APPROXIMATE TANDEM REPEATS OF K-K-E.
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                                                                                                                                      DB 1;
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                                                                                                                                                  Length 474;
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Result
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Maximum Match 100%
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Perfect score:
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Q9vg05 drosophila
O35807 rattus norv
O9h6q7 homo sapien
O91182 euglena gra
O91xr2 arabidopsis
O14347 schizosacch
O951v6 macaca fasc
O9p529 neurospora
O9h5v6 homo sapien
O64075 rattus sp.
O91gz9 arabidopsis
O9nt34 homo sapien
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# ALIGNMENTS

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Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	HOSTIN D., Houston K.A., Howland T.J., Wei MH., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke 2., Kennison J.A., Ketchum K.A.,		Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,	3	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I. Dietz S. M.		Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D. Bolshakov S.	Ballew R.M., Basu A., Baxendale J., Bayraktaroglii I. Beasley F M	Abril J.F., Agbayani A., An HJ., Andrews-Pfannkoch C., Baldwin D.	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R. Miklos G.L.G.	Brandon R.C., Rogers YH.C., Blazet R.G. Champe M. Dfeiffer B D	Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S. N.	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocavne J.D.,	MEDLINE-20196006; PubMed-10731132;	STRAIN-BERKELEY;	SEQUENCE FROM N.A.	[2]	NCBI_TaxID=7227;	Ephydroidea; Drosophilae; Drosophila.	ים	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	Drosophila melanogaster (Fruit fly).	CG7518.	EIN.	-2001 (TrEMBLrel. 17,	(TrEMBLrel. 16,	01-MAY-2000 (TrEMBLrel. 13, Created)		Q9VG05 PRELIMINARY: PRT: 2451 AA	05

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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Melson C.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Rubin G.M., Wenter J.C.;

"The genome sequence of Drossphila melanogaster.";

DR RMIL ABON3603. ABFS488 2.
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MEDLING-98172708; pubmed-9511718;
Proels F., Loser B., Marx M.;
Proels F., Loser B., Marx M.;
"Differential expression of osteopontin, PC species, during in vitro angiogenesis.";
Exp. Cell Res. 239:1-10(1998).
EMBL; V08769; CAA70022.1; -
InterPro; IPR000719; Euk_pkinase.
Pfam; PF00069; pkinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-bidding; Transferase.
SEQUENCE 129 AA; 15080 MW; 38102272BBE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O35807 PRELIMINARY; PRT; 129 AA.
O35807;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MICROVASCULAR ENDOTHELIAL DIFFERENTIATION PROTEIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
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F1yBase; FBgn0038108; CG7518.
InterPro; IPR001005; Myb_DNA_bind.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
SEQUENCE 2451 AA; 266959 MW; 088A2293F27481E2 CRC64;
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Pred. No. 0.014;
3; Mismatches
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Pred. No. 0.
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RESULT Q9LXR2

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Best Local
                                                                                                 Matches
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InterPro; IPR002478; PUA.
InterPro; IPR002501; TruB_N.
Pfam; PF01472; PUA; 1.
Pfam; PF01509; TruB_N; 1.
SMART; SM00359; PUA; 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA: FLJ21979 FIS, CLONE HEP06065 (FRAGMENT).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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Q9H6Q7;
Q1-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema !
Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Sl
Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human CDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK025632; BAB15196.1;
NON_TER 720 720
NON_TER 720 AA; 84029 MW; A86586FEAA953D0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09LL82; PRELIMINARY;
09LL82; O1-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                    "Evolutionary appearance of genes encoding proteins associated with box H/ACA snoRNAS: Cbf5p in Euglena gracilis, an early diverging eukaryote, and candidate Garlp and Nopl0p homologs in archaebacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-STREPTOMYCIN-BLEACHED STRAIN;
MEDLINE-20330353; PubMed-10871366;
                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watanabe Y., Gray M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euglena gracilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CBF5P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
     420
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AKKSITNSDIVSISKKKKKKKKKKKKKKKKKKKKK 711
                                                                                                                        Similarity
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                                                                                                                                                                                                                            467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euglenozoa;
                                                                                                 Conservative
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                                                                                                                                                                                                                            52385 MW;
                                                                                                                     48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.2%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                   Score 102; DB 1
Pred. No. 0.075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 105;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                       401089B66507BA7B CRC64;
                                                                                              Mismatches
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                                                                                                                                            DB 10;
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                                                                                            14;
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                                                                                                                                          Length 467;
  462
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                                                                                              Indels
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Best Local S
Matches 21
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Submitted (APR-2000) to the EI
EMBL; Ai353032; CAB88307.1; -
InterPro: IPR001810; F-box.
Pfam; PF00646; F-box; 1.
SMART; SM00256; FBOX; 1.
PROSITE: PS50181; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                      014347
014347;
01-JUN-1998
01-JUN-1998
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
D'Angelo M., Vezzi A., Modesto
D'Angelo M., Vezzi A., Mayer K.F.y
Rudd S., Lemcke K., Mayer K.F.y
Rudd S., Lemcke K., Mayer EMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09LXR2;
01-OCT-2000
01-OCT-2000
01-OCT-2001
                                Pfam; PF00226; DnaJ; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS00036; DNAJ 1: 1.
PROSITE; PS50076; DNAJ 2; 1.
Hypothetical protein; Chaperone;
                                                                                                         EMBL; Z97992; CAB10796.1; HSSP; P25685; 1HDJ.
                                                                                                                                                                   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases -!- FUNCTION: Z-DNA BINDING PROTEIN. COULD BE INVOLVED
                                                                                                                              ORGANIZATION (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY
-!- SIMILARITY: CONTAINS A DNAJ-LIKE
                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TREMBLIEL 06, Created)
01-JUN-1998 (TREMBLIEL 06, Last sequence update)
01-JUN-2001 (TREMBLIEL 17, Last annotation update)
PUTATIVE ZUOTIN-LIKE PROTEIN C30D10.01 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                        Hypothetical
NON_TER
                                                                                                                                                                                            Duesterhoeft A.;
                                                                                                                                                                                                        Wood V., Rajandream M.A.,
                                                                                                                                                                                                                                                                                     Schizosaccharcmyces pombe (Fission yeast).
Schizosaccharcmycetes;
Fukarvota: Fundi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                   SPBC30D10.01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eurosids II; Bra
NCBI_TaxID=3702;
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T20N10_250.
                                                                                                 InterPro;
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Similarity 80.8%;
21; Conservative
                                                                                            IPR001623; DnaJ_N
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(TrEMBLrel. 15, Last
(TrEMBLrel. 18, Last
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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 81
267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59689 MW;
                                                                                                                                                                                                                                                                             Schizosaccharomycetaceae;
                                                                                                                                           NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                      Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           project;
ne EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sto D., Pigazzi M., F.X., Quetier F., EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 102; DE
Pred. No. 0.08
0; Mismatches
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DNAJ-LIKE.
ALA/LYS-RICH
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                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EC6D957D01F86E70
                                  DNA-binding;
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                                                                                                                                  DOMAIN
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                                   Nuclear
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Salanoubat
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                                                                                                                                                                    IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      517;
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RESULT
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Q95LV6
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Best Loc
Matches
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Best Local
                 German Neurospora genome pro
Submitted (OCT-2001) to the
EMBL; AL356815; CAB92638.2;
                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HYPOTHETICAL 15.2 KDA PROTEIN.
B24H17.160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q95LV6;
                                                                            SEQUENCE FROM N.A. Schulte U., Aign V., Nyakatura G., Mewes
 Hypothetical protein SEQUENCE 128 AA;
                                                                                                                                       Neurospora crassa.
Eukaryota; Fungı;
                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
NON_TER 531 53
SEQUENCE 531 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-2001) to the EMBL; AB071085; BAB64479.1;
                                                                                                                                                                                                                                                                                                                                                                                                             Terao K., Sugano S.;
"Isolation of novel full-length libraries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca fascicularis (Crab eating macaque) (Cynomolgus monk
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                SEQUENCE FROM N.A.
                                                                     Submitted
                                                                                                                    NCBI_TaxID=5141;
                                                                                                                               Sordariales;
                                                                                                                                                                                                             Q9P529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-TESTIS;
Hashimoto K., Osada N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae; Macaca.
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
HYPOTHETICAL 61.4 KDA PROTEIN (FRAGMENT).
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20; Conserv
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                                                                    (MAY-2000)
                                                                                                                             Fung1; Ascomycota;
s; Sordariaceae; Net
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                                                                                                                                                                                                 (TrEMBLrel.
                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                              Conservative
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15157
                                                                                                                                                                                                                                                                                                                                                               61389
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                                                                                                                                                                                                                                                                                                                      48.3%;
95.2%;
                                                                          Hoheisel J., Brandt
H.W., Mannhaupt G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hida M., Kusuda
                           project;
the EMBL/GenBank/DDBJ
MW.
                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                             Neurospora
                                                                                                                                                                                                                                                                                          45
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                                                                  EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                      Score 101;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 101.5; DB Pred. No. 0.064; Mismatches
                                                                                                                                        Pezizomycotina;
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
8C7C65C3DFB70765 CRC64;
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                                                                                     Fartmann B.,
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                            databases
                                                                   databases
                                                                                                                                        Sordariomycetes
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                                                                                      Holland
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NCBI_TaxID=9606;
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O9H5V6; PRESIDENT OF THE PROPERTY OF THE PROP
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SEQUENCE
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
NUCLEOPORIN P62 HOMOLOG
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EMBL; S75997; AAB33384.1;
                                                                                                                                                                                                                                                      "An unusual nucleoporin-related messenger ribonucleic acid is in the germ cells of rat testis.";
Biol. Reprod. 51:1022-1030(1994).
EMBL; S75997; AAB33384.1; -.
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95151924; PubMed=7849178; Wang Z.Q., Akmal K.M., Kim K.H.;
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TISSUE=TESTIS;
Ottenwaelder B., Obermaier B., M
submitted (JAN-2000) to the EMBL
EMBL: AL137556; CAB70810.1; -.
Hypothetical protein.
NON_TER 380 380
SEQUENCE 380 AA; 42689 MW; 6
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"Structural Analysis of Arabidopsis thaliana Chromosome Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002460; BAA97098.1; -.
InterPro; IPR001386; Linker_histone.
PRINTS; PR00624; HISTOMEH5.
PRINTS; PR00624; HISTOMEH5.
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OSIGZ9:
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 17, Last sanotation update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, BAC CLONE:F1D9.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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HYPOTHETICAL 42.7 KDA PROTEIN (FRAGMENT).
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Best Local S
Matches 23
                                                                                                        Query Match
Best Local
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Interpro; IPRO02110; ANK.
Pfam; PF00023; ANK; 14.
SMART; SM00248; ANK; 14.
PROSITE; PS50088; ANK_REPEAT; 13.
PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                              ANK repeat; Repeat.
NON_TER 686
SEQUENCE 686 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "NEDO human cDNA sequencing Submitted (FEB-2000) to the EMBL; AK000295; BAA91063.1;
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Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Mat Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Oba Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ20288 FIS, CLONE HEP04414 (FRAGMENT).
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InterPro: IPR0001304; lectin_c.
InterPro: IPR0001304; lectin_c.
InterPro: IPR0001306; znf_FYVE.
Pfam; PF01363; FYVE; 1.
PRINTS; PR00308; ANTIFREEZEI
SMART; SM00064; FYVE; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
PROSITE; PS00615; AN; 43414 MW; 180C2F1DF47C55D7
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Eukaryota; Euglenozoa;
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                                                                           l Similarity
21; Conserv
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73615 MW; AE1380212E0FAD22 CRC64;
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48.9%;
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                                                                 Score 99; DB Pred. No. 0.19
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EMBL/GenBank/DDBJ databases
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T., Sugano S.;
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Q9HC48;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CTCL TUMOR ANTIGEN SE2-5 (FRAGMENT).
                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001478; PDZ. Pfam; PF00595; PDZ; 2. SMART; SM00228; PDZ; 2. PROSITE; PS50106; PDZ; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21143360; PubMed=11149944; Eichmuller S., Usener D., Dummer R Schadendorf D.;
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648 RKKKKKKKKKKKKKKKKKK 667
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Soluble tandem pEA AsK21 linker pepti Modified fibre pro Modified fibre pro Drosophila melanog Human polypeptide Human polypeptide Human polypeptide Human polypeptide Novel human diagno Soluble peptide an Nuclear ligand use
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AAO08095 ABG26720 AAO03024 AAO03024 AAU18205 AAU18277 AAY8248 AAU23799 AAB59105 AAV12950 AAV12950 AAV12950 AAV12950 AAV12950 AAV12950 AAV12950 AAV12950 AAV12950 AAV12950 AAV12950 AAV12950 AAV12950 AAV18178 AAV07505	AAY59040 AAU04285 AAB45848 AAO03278 AAO089437 AAO02477 AAU18240 AAO1105 AAO02246 AAO02246 AAO08947 AAU08197 AAU08197 AAU08197 AAU08197
	Nuclear ligand for Nuclear ligand #2 Nucleic acid trans Human polypeptide Human polypeptide Novel human polypeptide Novel human DNA-bi Human polypeptide Novel human DNA-bi Human polypeptide

## ALIGNMENTS

AAB13783 RESULT

AAB13783 standard; peptide; 45 AA

AAB13783;

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Antigens modified by the covalent addition of a peptide that facilitates entry into antigen presenting cells, useful for producing compositions for immunizing against tumors and pathogens -  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-442365/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hakim I, Vidovic
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pk peptide; cytostatic; vaccine; cytotoxic T cell; CTL; immunotherapy; major histocompatibility complex class 1; MHC class 1; antigen; tumour; prostate; breast; multiple myeloma; pEA peptide.

Soluble tandem pEA/ pK peptide conjugate

10-NOV-2000 (first entry)

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RESULT
AAB23585
ID AAB2
XX AAB2
AX AAB2
AX AAB2
XX Vira
DE ASK2
XX Vira
KW tumc
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                                             This invention relates to a viral vector constructed by the fusion of a viral protein with a ligand which binding specifically to the melanocyte-stimulating hormone (MSH) receptor. The vector contains one of four linkers represented by sequences AAA93815-A93818 and AAB25387-B23586, and DNA encoding a fibre protein selected from those represented by AAA93819-A93826 and AAB25387-B23594. The vector has cytostatic activity, and can be used for gene therapy and in the viagnosis and treatment of tumours, particularly malignant melanomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Virus vector useful in diagnosis and treatment of tumors particularly malignant melanoma, constructed by fusing viral protein with ligand binding specifically to melanocyte-stimulating hormone receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-549414/50.
N-PSDB; AAA93817.
                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 100; 145pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour; malignant melanoma; linker
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Pred. No. 1.4e-14;
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                                                                                                                              This invention relates to a viral vector constructed by the fusion of a viral protein with a ligand which binding specifically to the melanocyte-stimulating hormone (MSH) receptor. The vector contains one of four linkers represented by sequences AAA93815-A93818 and AAB23583-B23586, and DNA encoding a fibre protein selected from those represented by AAA93819-A93826 and AAB23587-B23594. The vector has cytostatic activity, and can be used for gene therapy and in the diagnosis and treatment of tumours, particularly malignant melanomas. The present sequence represents a modified fibre protein used in the construction of the vector.
                                                                                                                                                                                                                                                                                     Virus vector useful in diagnosis and treatment of tumors particularly malignant melanoma, constructed by fusing viral protein with ligand binding specifically to melanocyte-stimulating hormone receptor -
                                                                                                           Sequence
                                                                                                                                                                                                                                                                Claim 24; Page 121-126; 145pp; Japanese.
                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viral vector; melanocyte-stimulating hormone receptor; MSH; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour; malignant melanoma; fibre protein
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DB; AAA93823.
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                                                Conservative
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                                                            56.9%;
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                                                5.
                                               Score 119; DB 21;
Pred. No. 0.00016;
5; Mismatches 5
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Pred. No. 1e-05;
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     WO200171042-A2
                    Drosophila melanogaster
                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                 Drosophila
                                                                                                                                                                                                                                                                                                                                                                          Virus vector useful in diagnosis and treatment of tumors particularly malignant melanoma, constructed by fusing viral protein with ligand binding specifically to melanocyte-stimulating hormone receptor
                                       pharmaceutical.
                                                                                  26-MAR-2002
                                                                                                                    ABB71574 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                          Claim 24; Page 131-136; 145pp; Japanese.
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                             construction of the
                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                              tumour; malignant melanoma; fibre protein.
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DB; AAA93825.
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                                                               melanogaster polypeptide
                                                                                                                                                                                                                                              640
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Pred. No. 0.00016;
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        (HYSE-) HYSEQ INC
                                                                   07-SEP-2001
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28-FEB-2000;
18-MAY-2000;
                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; vaccine; peptide therapy; stem cell growth factor; haematc tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1374 aaaaaeaaaaaeaaaaaaaaaeaaaeqkaklknkkqakk 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL10151), expressed DNA sequences (ABL101840-ABL10151) and the encoded proteins (ABB57737-ABB72072).
                                                                         26-FEB-2001; 2001WO-US04927
                                                                                                                                                                         WO200164835-A2
                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 15260
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N-PSDB; ABL15677.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAAEAAAAAAEAAAAAAKKKKKKKKKKKKKK 39
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actions -
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28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein; 123
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2000US-0515126
2000US-0577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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2000US-0614150
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75.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 118; DB 22;
Pred. No. 0.00072;
3; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                 cell differentiation; gene therapy;
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format directly from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
diagnosing and treating e.g.
                                                                                                                                                                                                                                                                                         28-FEB-2000;
18-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide SEQ ID NO 17595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAO03703 standard; Protein; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment of cancer, leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g.\ leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lagnosing and treating e.g.
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                                                                                               2001-514838/56
DB; AAI83634.
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27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI81299
                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 on relates to human polynucleotides (AAI799 proteins (AAO00010-AAO13910) that exhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                         2000US-0515126
2000US-0577409
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Pred. No. 7.3e-05
5; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AAI79941-AAI93841) and
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AC AAU1
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Best Local
18 - APR - 2000

19 - KAY - 2000

07 - JUN - 2000

28 - JUN - 2000

30 - JUN - 2000

07 - JUL - 2000

11 - JUL - 2000
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; DNA-binding protein; histone; chromo domain protein; chromatin organisation modifier; Y-box binding protein; DNA organisation; gene transcription; malignant disease; autoimmune disorder; rheumatic disease; genetic abnormality; infectious disease; neurological disorder; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunomodulatory; anti-HIV; anti rheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation.
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26; Conserv
2000US-0205515.
2000US-020467.
2000US-0214886.
2000US-0215135.
2000US-0216647.
2000US-0217487.
2000US-0217496.
2000US-0217496.
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2000US-0190076.
2000US-0198123.
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70.3%;
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Pred. No. 7.6e-05;
0; Mismatches 11
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Gaps

14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000;

3-JUL-2000; 6-JUL-2000; 4-AUG-2000; 4-AUG-2000; 4-AUG-2000;

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The present invention relates to the isolation of novel DNA-binding proteins, and cDNA (AAS29030-AAS29157) and genomic sequences encoding for these proteins. DNA-binding proteins such as histones, chromo (chromatin organisation modifier) domain proteins, and y-box binding proteins may contribute to diseases resulting from aberrant DNA organisation and/or gene transcription. The sequences of the invention are useful in screening assays to identify antagonists and/or agonists that may enhance or block activities mediated by DNA-binding proteins. Blockers of DNA-binding proteins may be useful in treating disorders such as malignant diseases (e.g. cancer), autoimmune disorders (e.g. diabetes mellitus), rheumatic diseases (e.g. rheumatoid arthritis), genetic abnormalities (e.g. cystic fibrosis), infectious
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01-DEC-2000
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09 - NOV - 2000

01 - N
                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                       Nucleic
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DB; AAS29151.
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                                                                                                                                                                                                                                                                                                                                                                                  acid
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2000US-0246523.
2000US-0246524.
2000US-0246526.
2000US-0246528.
2000US-0246528.
2000US-0246611.
2000US-0246611.
2000US-0249210.
2000US-0249211.
2000US-0249211.
2000US-0249211.
2000US-0249212.
2000US-0249214.
2000US-0249214.
2000US-0249215.
2000US-0249214.
2000US-0249215.
2000US-0249216.
2000US-0249266.
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2000US-0251198.
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2000US-0246476.
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2000US-0224511
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RESULT
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Best Loc
Matches
                            polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating insign of sites expressing (II). (I) and (II) are useful for treating the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications of the polypeptide and polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases (e.g. HIV) and neurological disorders (e.g. Alzheimer's disease). The polynucleotide sequences of the invention may also be used in gene therapy. AAU18154-AAU18281 represent novel DNA-binding
                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 57077; 103pp; English
                                                                                                                                                                                                                                                                                                                                                           biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #26709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adslaaswqvaemvelekkkkkkkkkkkkkkkkkkkkkk 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome mapping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
forensics, gene mapping, identification of mutations or genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                         relates to isolated polynucleotide (I) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e mapping; gene mapping; gene therapy; forensic
medical imaging; diagnostic; genetic disorder.
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Pred. No. 0.00011;
2; Mismatches 13
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                                                                                                                                                                                                                                                                                                                                                                                                mutations
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Similarity 25; Conserv

52.2%; but 100.0%; Pr ... 0;

Score 109; DB 21; Pred. No. 7.1e-05; Pred. No. 7.1e-05;

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Best Local
                      The present invention relates to compositions of modified soluble protein antigens capable of eliciting an enhanced in vivo cytotoxic T cell (CTL) response i.e. a major histocompatability complex (MHC) class I molecule response. The protein antigen is modified by the covalent addition of a peptide sequence which facilitate entry of the antigen into antigen presenting cells (APCs). The present sequence is one such peptide sequence which can be used to modify the soluble antigens. The present sequence is peptide pEA. The modified antigen composition may be used for immunising against, or treating a tumour e.g. prostate and breast carcinoma or multiple myeloma, or pathogen in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and to produce other types of data and products dependent on I amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                  Antigens modified by the covalent addition of a peptide that facilitates entry into antigen presenting cells, useful for compositions for immunizing against tumors and pathogens -
                                                                                                                                                                                                                                                                                     Laus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pEA peptide; cytostatic; vaccine; cytotoxic T cell; major histocompatibility complex class 1; MHC class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                (DEND-)
                                                                                                                                                                                                                                                                                                                                         14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                    14-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                      WO200035949-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB13781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB13781 standard; peptide;
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                                                                                                                                                                                                                                                                                                                DENDREON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
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                                                                                                                                                                                                                                                                                    Hakim I, Vidovic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          breast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                         98US-0112324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen pEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.6%;
                                                                                                                                                                                                                                                                                     D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTL; immunotherapy;
1; antigen; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 on DNA
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В
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                                                                                                                                    The present invention relates to a transporter system for delivering CC nucleic acid to a cell. The system comprises a nucleic acid binding CC complex, consisting of a binding molecule bonded non-covalently to the CC nucleic acid, and covalently to a surface ligand, and a lytic agent. The CC binding molecule is spermine or a spermidine derivative. Nucleotide CC sequences AAA36633-A36652 and peptide sequences AAY98456-Y98500 are used in the construction of the transporter system of the invention. The CC transporter system is used in gene therapy, particularly to deliver CC nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g CC for treating cardiovascular disease, cancer, and infection. The CC transporter systems are also used to create transgenic animals (as models include transforming cells to produce proteins, or transfecting cells in CC vitro to study the function of the nucleic acid. The use of a surface CC ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular cc interior, from endosomes, without requiring endosomal or lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
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                                                        Query Match
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Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent
                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Column 123-124; 108pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transporter system;
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19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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 12
                            20 EAAAAKKKKKKKKKKKKKKKKKK 45
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                                                                         Similarity
                                                                                                                                    59
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92US-0855389
93WO-US02725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tem; nucleic acid delivery; gene the cardiovascular disease; infection.
                                                                      52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in nucleic acid transporter system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cristiano RJ,
                                                         0;
                                                                      Score 109; DB 21;
Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Woo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLC,
                                                                                  Length 59;
                                                        Indels
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                                                        0,
                                                      Gaps
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RESULT

В Š

AAU04285 standard;

Peptide;

59

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AAY59040
ID AAY5
                                                                                                                                                                                                                                                                                                                                 The invention relates to a nucleic acid transport system (NTS) for CC delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; CC (b) a moiety that recognizes and binds to a cell surface receptor or CC antigen or is capable of entering a cell through cytosis; (c) a nucleic cacid or macromolecular molecule binding molety; (d) a molety that is CC capable of moving or initiating movement through a nuclear membrane; and/CC or (e) a lysis molety that enables the transport of the entire complex CC from the cell surface directly into the cytoplasm of the cell. The NTS CC delivers nucleic acid into the cellular interior as well as the nucleus of specific nucleic acid accordingly. The NTS can also be used to create CC transgenic animals for assessing human disease, such as cancer, in an CC animal model. The NTS can be used in vitro with tissue culture cells complex complex the role of various nucleic acids to be studied by targeting complex in the transport with the contraction of the cells. The NTS can be used to create the contraction of the cells and the contraction of the cells capable of various nucleic acids to be studied by targeting contraction into specifically targeted tissue culture cells. The CC lysis agent within the NTS avoids the problem of endosomal/lysosomal contractions.
                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
14-DEC-1993;
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Columns 119-122; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nuclear membrane; lysis moiety; transgenic animal; nucleic acid delivery; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid transport system;
nuclear membrane; lysis moiety;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-038262/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2000
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                           20 EAAAAKKKKKKKKKKKKKKKKKKKK 45
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92US-0855389.
93WO-US02725.
93US-0167641.
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                                                                                                                                          52,2%;
88,5%;
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                                                                                                                                          Score 109; DB 21; Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTS; cell surface receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ⋧
37
                                                                                                               Mismatches
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                                                                                                                                                                  21;
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                                                                                                                                                                  Length 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith
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Best Local S
Matches 23
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20-MAR-1992;
19-MAR-1993;
                                                                                                                                          growth factor; clotting factor; apolipoprotein; tumor antigen; tumor suppressor; viral antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents the nuclear ligand, #2, used in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules are used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells.
                                                                     inidentified
                                                                                                                     bacterial antigen
                                                                                                                                                                                Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme;
                                                                                                                                                                                                                                        Nucleic acid transporter system
                                                                                                                                                                                                                                                                                              21-MAR-2001
                                                                                                                                                                                                                                                                                                                                            AAB45848
                                                                                                                                                                                                                                                                                                                                                                                          AAB45848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WOO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear ligand #2 used in nucleic acid transporter system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BAYU ) BAYLOR COLLEGE MEDICINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leic acid transport system, useful for creating transgenic assessing human disease such as cancer in an animal model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAAAAKKKKKKKKKKKKKKKKKK 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Column 8; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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92US-0855389.
93WO-US02725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0462040
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                                                                                                                                                                                                                                                                                                                                                                                          Protein;
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                                                                                                                                                                                                                                                                                                                                                                                          59
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                          A
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                                                                                                                                                                                                                                        peptide ligand
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bone forming cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        00016;
                                                                                                                                                                                                                                        SEQ
                                                                                                                                     receptor; drug; on parasitic antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 59;
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                                                                                                                                                            oncogene;
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to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid. The nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, applipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor suppressors, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
Sequence
                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                               Disclosure; Column 123-124; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BAYU ) BAYLOR COLLEGE MEDICINE
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                                                                                                                                                                                                                                                                                             invention describes a novel system (I) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-049093/06
59
ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sparrow
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92US-0855389.
93WO-US02725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cristiano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith
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                                                                                                                                                                                                                                                                                             nucleic
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Matches
                          Best Local
                                 Query Match
20 EAAAAKKKKKKKKKKKKKKKKKK 45
                Similarity
23; Conserv
                Conservative
                       52.2%;
               Score 109; DB Pred. No. 0.00 0; Mismatches
                0
                       DB 22;
                               Length
                Indels
                                 59
                0
               Gaps
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12
eapykakkkkkkkkkkkkkkkkkk 37
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RESULT
                                            06-NOV-2001
                                                 AA003278
                                                     AAO03278 standard; Protein;
                                           (first entry)
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Human polypeptide

SEQ ID NO 17170.

Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation. WO200164835-A2 Homo sapiens

07-SEP-2001

26-FEB-2001; 2001WO-US04927

28-FEB-2000; 18-MAY-2000; 2000US-0515126 2000US-0577409

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                                                                                                                                                  Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                             The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine. Cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, insunnomodulatory activity and activity in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-514838/56.
N-PSDB; AAI83209.
                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 17170; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                              36 aligalravaqkkkkkkkkkkkkkkkkkk 66
                                                                                                                15 AAAAAEAAAAKKKKKKKKKKKKKKKKKKK 45
                                                                                                                                                                                                                                    74 AA;
                                                                                                                                           Conservative 0; Mismatches
              1, 2002, 06:19:25
                                                                                                                                                                  52.2%;
77.4%;
                                                                                                                                                                Score 109; DB 22;
Pred. No. 0.0002;
                                                                                                                                                                              Length 74;
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 s
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB
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243
1 CGLEGAIAGFIENGWEGMID.....KKKKKKKKKKKKKKKKKKKKKK 44
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hemagglutinin

## ALIGNMENTS

A;Cross-references: GB:M19057; NID:g324210 A;Note: the sequence in GenBank entry FLAHAPB, C;Genetics: C;Accession: B29971
R;Kida, H.; Shortridge, K.F.; Webster, R.G.
Virology 162, 160-166, 1988
A;Title: Origin of the hemagglutinin gene of H3N2 influenza
A;Reference number: A94370; MUID:88101364
A;Accession: B29971 hemagglutinin precursor - influenza A virus (strain A/swine/81/78) (fragment) C;Species: influenza A virus C;Date: 13-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 18-Sep-1998 A; Molecule type: genomic A; Residues: 1-550 <KID> A:Map position: segment 4
C:Superfamily: influenza virus hemagglutinin
C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester
F:1-328/Product: hemagglutinin HA1 #status predicted <HA1> A; Molecule type: genomic RNA A; Residues: 1-550 <KID> A; Cross-references: GB:M19056; NID:g324208 A; Note: the sequence in GenBank entry FLAHAPA, C; Genetics: C;Accession: A29971
C;Accession: A29971
C;Accession: A29971
R;Kida, H.; Shortridge, K.F.; Webster, R.G.
Virology 162, 160-166, 1988
A;Title: Origin of the hemagglutinin gene of H3N2 influenza viruses from pigs in Chin A;Reference number: A94370; MUID:88101364
A;Accession: A29971 밁 Ş F;330-550/Product: hemagglutinin HA2 \*\*status predicted <HA2>
F;520-536/Domain: transmembrane \*\*status predicted <TMI>
F;8.22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) \*\*status F;14-466,52-277,64-76,139-473,281-305/Disulfide bonds: \*\*status predicted F;539,546,549/Binding site: palmitate (Cys) (covalent) \*\*status predicted C:Species: influenza A virus C:Date: 31-Mar-1989 \*sequence\_revision RESULT HMIVS2 hemagglutinin precursor - influenza A virus (strain A/swine/126/82) (fragment) Matches Query Match
Best Local Similarity N genomic RNA Conservative 55.1%; 100.0%; 0, Score 134; Pred. No. Mismatches 31-Mar-1989 #text\_change 18-Sep-1998 3.1e-06; hes 0; DB 1; release 106, (PID:g324211) differs fro release 106, Length 550 Indels viruses (PID:g324209) d1ffers 0, from Gaps pigs 0 bond 'n Chin fro

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hemagglutinin precursor - influenza A virus (strain A/duck/Hokkaido/5/77) (fragment)
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Jun-1989 *sequence_revision 30-Jun-1989 *text_change 16-Jul-1999
C;Accession: A27813
R;Kida, H; Kawaoka, Y; Naeve, C.W.; Webster, R.G.
Virology 159, 109-119, 1987
A;Title: Antigenic and genetic conservation of H3 influenza virus in wild ducks.
A;Reference number: A94363; MUID:87265458
A;Accession: A27813
A;Mclecule type: genomic RNA
A;Residues: 1-550 <KID>
A;Cross -references: GB:M16737; NID:g324081; PIDN:AAA43143.1; PID:g324082
C;Genetics:
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-328/Product: hemagglutinin HA1 *status predicted <HA1>
F;30-536/Domain: transmembrane *status predicted <HA1>
F;8.720-336/Domain: segment *Status predicted <HA1>
F;8.720,336-52-277,64-76,139-473,281-305/Disulfide bonds: *status predicted
F;34-466,52-277,64-76,139-473,281-305/Disulfide bonds: *status predicted
F;34-546,549/Binding site: palmitate (Cys) (covalent) *status predicted
F;339,546,549/Binding site: palmitate (Cys) (covalent) *status predicted
HMIV80

HMIV80

Hemagglutinin precursor - influenza A virus (strain A/duck/Hokkaido/8/80) (fragment)

N;Contains: hemagglutinin HAI; hemagglutinin HA2

C;Species: influenza A virus

C;Decies: influenza A virus

C;Accession: B27813

R;Kida, H.; Kawaoka, Y.; Naeve, C.W.; Webster, R.G.

Virology 159, 109-119, 1987

A;Title: Antigenic and genetic conservation of H3 influenza virus in wild ducks.

A;Reference number: A94363; MUID:87265458

A;Accession: B27813

A;Molecule type: genomic RNA

A;Residues: 1-550 <KID>

A;Cross-references: GB:M16738; NID:g324083

A;Note: the translation in Fig. 2 is inconsistent with the nucleotide sequence in Fig. C;Genetics:
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C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester
C;Keywords: glycoprotein; hemagglutinin HAI *status predicted <HAI>
F;1-328/Product: hemagglutinin HA2 *status predicted <HA2>
F;300-550/Product: hemagglutinin HA2 *status predicted <TMI>
F;520-556/Domain: transmembrane *status predicted <TMI>
F;8,22,38,165,285,483/Bhinding site: carbohydrate (Asn) (covalent) *status predicted
F;14-466,52-277,64-76,139-473,281-305/Disulfide bonds: *status predicted
F;539,546,549/Binding site: palmitate (Cys) (covalent) *status predicted
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A:Map position: segment 4
C:Superfamily: influenza virus hemagglutinin
C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester l
F:1-328/product: hemagglutinin HA1 *status predicted <HA1>
F:130-550/product: hemagglutinin HA2 *status predicted <HM1>
F:330-550/product: hemagglutinin HA2 *status predicted <HM1>
F:520-536/Domain: transmembrane *status predicted <HM1>
F:62.23,18,165,285,483/Binding site: carbohydrate (Asn) (covalent) *status predicted
F:14-466,52-277,64-76,139-473,281-305/Disulfide bonds: *status predicted
F:539,546,549/Binding site: palmitate (Cys) (covalent) *status predicted
A:Cross-references: GB:M16740;
C;Genetics:
A;Map position: segment 4
                                                                                                                                   hemagglutinin precursor - influenza A virus (strain A/duck/Hokkaido/7/82) (fragment) N;Contains: hemagglutinin HA1; hemagglutinin HA2 C;Species: influenza A virus C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999 C;Accession: D27813 R;Kida, H.; Kawaoka, Y.; Naeve, C.W.; Webster, R.G. Virology 159, 109-119, 1987 Virology 159, 109-119, 1987 A;Title: Antigenic and genetic conservation of H3 influenza virus in wild ducks. A;Reference number: A94363; MUID:87265458 A;Accession: D27813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Map position: segment 4
C:Superfamily: influenza virus hemagglutinin
C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolest
F:1-328/Product: hemagglutinin HA1 #status predicted <HA1>
F:330-550/Product: hemagglutinin HA2 #status predicted <HA2>
F:330-556/Demain: transmembrane #status predicted <TM1>
F:520-536/Domain: transmembrane #status predicted <TM1>
F:8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status
F:14-466,52-277,64-76,139-473,281-305/Disulfide bonds: #status predicted
F:539,546,549/Binding site: palmittate (Cys) (covalent) #status predicted
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A:Title: Antigenic and genetic conservation of H3 influenza virus in wild ducks. A;Reference humber: A94363; MUID:87265458
A;Accession: C27813
                                                                                         A; Molecule type: genomic RNA
A; Residues: 1-550 <KID>
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C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: C27813
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N;Contains: hemagglutinin HA1; hemagglutinin HA2
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                                                     PID: g324088
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A; Map position: segment 4
C: Superfamily: influenza virus hemagglutinin
C: Keywords: glycoprotein; hemagglutinin; homm
                                                                                                                               Virology 159, 109-119, 1987
A;Title: Antigenic and genetic conservation
A;Reference number: A94363; MUID:87265458
A;Accession: F27813
A;Molecule type: genomic RNA
A;Residues: 1-550 <KID>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Superfamily: influenza virus hemagglutinin
C:Keywords: glycoprotein; hemagglutinin; homotrimer
F;1-328/Product: hemagglutinin HA1 #status predicted <HA1>
F;310-550/Product: hemagglutinin HA2 #status predicted <HA2>
F;320-555/Pomain: transmembrane #status predicted <TM1>
F;7.8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;14-466,52-277,64-76,139-473,281-305/Disulfide bonds: #status predicted
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C;Reywords: glycoprotein; hemagglutinin; thiolest
F;1-328/product: hemagglutinin HAI #status predicted <HAI>
F;330-550/Product: hemagglutinin HA2 #status predicted <HA2>
F;530-536/Domain: transmembrane #status predicted <TMI>
F;8.22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status F;14-466,52-277,64-76,139-473,281-305/Disulfide bonds: #status predicted
F;539,546,549/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                  A;Cross-references: GB:M16742;
C;Genetics:
                                                                                                                                                                                                                                                      C;Accession: F278L3
R;Kida, H.; Kawaoka, Y.; Naeve, C.W.; Webster, R.G.
                                                                                                                                                                                                                                                                                                                              hemagglutinin precursor - influenza A virus (strain N;Contains: hemagglutinin HA1; hemagglutinin HA2 C;Species: influenza A virus C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989
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A;Title: Antigenic and genetic conservation of H3 i A;Reference number: A94363; MUID:87265438
A;Accession: E27813
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A; Residues: 1-550 < KID>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Sep-1998
C;Accession: E27813
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N;Contains: hemagglutinin HA1; hemagglutinin HA2
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Best Local S
Matches 23
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Best Local S
Matches 23
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glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester
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100.0%;
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                                                                                                          NID: g324091
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; Pred. No. 3.
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n HA2
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A;Cross-references: GB:D00929; NID:g221279; PIDN:BAA00769.1; A;Note: the authors translated the codon GGG for residue 218 A;Note: residues 528-532 are not shown in this publication C;Superfamily: influenza virus hemagglutinin C;Keywords: glycoprotein; homotrimer F;1-328/Product: hemagglutinin HAl #status predicted <HAl>
                                                                                                                                                                                              C;Accession: JQ1153
R;Yasuda, J; Shortridge, K.F.; Shimizu, Y.; Kida, H.
J. Gen. Virol. 72, 2007-2010, 1991
A;Title: Molecular evidence for a role of domestic ducks
A;Reference number: JQ1153; MUID:91341491
A;Accession: JQ1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolest
F;1-328/product: hemagglutinin HAI #status predicted <HAI>
F;330-550/product: hemagglutinin HA2 #status predicted <HA2>
F;330-550/product: hemagglutinin HA2 #status predicted <TMI>
F;820-536/Domain: transmembrane #status predicted <TMI>
F;8.22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status
F;8-22,38,165,285,483/Binding site: palmitate (Cys) (covalent) #status predicted
F;539,546,549/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                               hemagglutinin precursor - influenza A virus (strain A/duck/Hong Kong/7/75) (fragment) N;Contains: hemagglutinin HA1; hemagglutinin HA2 C;Species: influenza A virus C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
JQ1153
                                                                                                                                                              A; Molecule type: genomic RNA
A; Residues: 1-550 < YAS>
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R;Kida, H.; Kawaoka, Y.; Naeve, C.W.; Webster, Virology 159, 109-119, 1987
A;Title: Antigenic and genetic conservation of A;Reference number: A94363; MUID:87265458
A:Accession: G27813
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F;330-550/Product: hemagglutinin HA2 *status predicted <HA2>
F;330-536/Domain: transmembrane *status predicted <TM1>
F;8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) *status F:14-466,52-277,64-76,139-473,281-305/Disulfide bonds: *status predicted F;539,546,549/Binding site: palmitate (Cys) (covalent) *status predicted
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: genomic RNA
A; Residues: 1-550 <KID>
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Pred. No.
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Pred. No.
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                                                                                                                                   PID: 9221280
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                                                                                                                                                                                                                                                              avian
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RESULT 11

JO1154
hemagglutinin precursor - influenza A virus (strain A/goose/Hong Kong/10/76) (fragment)
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Jun-2000
C;Accession: JO1154
R;Yasuda, J; Shortridge, K.F; Shimizu, Y; Kida, H.
J. Gen. Virol. 72, 2007-2010, 1991
A;Title: Molecular evidence for a role of domestic ducks in the introduction of avian H3
A;Reference number: JO1153; MUID:91341491
A;Accession: JO1154
A;Molecule type: genomic RNA
A;Residues: 1-550 <YAS>
A;Cross-references: GB:D00930; NID:9221273; PIDN:BAA00770.1; PID:9221274
A;Note: the authors translated the codon GGG for residue 218 as Glu
A;Note: residues 528-532 are not shown in this publication
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; homotrimer
F;1-328/Product: hemagglutinin HA1 #status predicted <HA1>
F;330-545/Product: hemagglutinin HA2 #status predicted <HA1>
F;8,22,38,165,285,483/Binding site: carbobydrate (Asn) (covalent) #status predicted
                                                                                                                                            hemagglutinin precursor - influenza A virus (strain A/duck/Hong Kong/64/76) (fragment)
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Jun-2000
C;Accession: JQ1155
R;Fasuda, J; Shortridge, K.F.; Shimizu, Y.; Kida, H.
J. Gen. Virol. 72, 2007-2010, 1991
J. Gen. Virol. 72, 2007-2010, 1991
A;Title: Molecular evidence for a role of domestic ducks in the introduction of avian H3
A;Reference number: JQ1153; MUID:91341491
A;Accession: JQ1155
A;Molecular type: genomic RNA
A;Residues: 1-550 <YAS>
A;Cross-references: GB:D00931; NID:9221277; PIDN:BAA00771.1; PID:9221278
A;Note: the authors translated the codon GGG for residue 218 as Glu, GCC for residues: Note: residues 528-532 are not shown in this publication
C;Keywords: glycoprotein; homotrimer
F;1-328/Product: hemagglutinin HA1 #status predicted <HA1>
F;3-30-545/Product: hemagglutinin HA2 #status predicted <HA2>
F;8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status predicted
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55.1%; Score 134; DB 2; 100.0%; Pred. No. 3.1e-06; tive 0; Mismatches 0;
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A;Title: Antigenic drift between the haemagglutinin of the Hong Kong influenza A;Reference number: A99231; MUID:80254693
A;Recession: A99231
A;Accession: A99231
A;Molecule type: genomic RNA
A;Residues: 1-566 <VER>A;Cross references: CB:J02090; NID:g324131; PIDN:AAA43178.1; PID:g324132
C;Csuperfamily: influenza virus hemagglutinin
C;Keywords: hemagglutinin; homotrimer; lippprotein; thiolester bond
E;1-16/Domain: signal sequence #status predicted <SII>F;17-344/Product: hemagglutinin HAI #status predicted <HAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hemagglutinin precursor - influenza A virus (strain A/Aichi/2/68)
k;Contains: hemagglutinin HAL; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 16-Jul-1999
C;Accession: A93231; A04051
R;Verhoeyen, M.; Frang, R.; Min Jou, W.; Devos, R.; Huylebroeck, D.; Saman, I
Nature 286, 771-776, 1980
A;Title: Antigenic drift between the haemagglutinin of the Hong Kong influence approximation of the Hong influence approximation of the Hong influence approximation of the Hong 
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A;Title: Cloning and DNA sequence of double-stranded copies of haemagglutinin genes A;Reference number: A93233; MUID:81030852
A;Accession: A93233
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A; Residues: 1-566 <BOT>
A; Cross references: GB: V01103
A; Cross references: GB: V01103
A; Experimental source: strain A/NT/60/68/29C
A; Note: human influenza strain A/NT/60/68/29C is a laboratory-isolated varia; Dophelde, T.A.; Ward, C.W.
R; Dophelde, T.A.; Ward, C.W.
A; Title: The disulphide bonds of a Hong Kong influenza virus hemagglutinin.
A; Reference number: A91276; MUID:80179105
A; Contents: annotation; disulfide bonds
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A;Accession: A93705
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Pred. No.
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hemagglutinin precursor - influenza A virus (strain A/Mem/102/72)

N.Contains: hemagglutinin HA1; hemagglutinin HA2

C;Species: influenza A virus

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 31-Mar-2000

C;Accession: A94441; A04051

R;Sleigh, M.J; Both, G.W.; Brownlee, G.G.; Bender, V.J.; Moss, B.A.
in Structure and Variation in Influenza Virus, Laver, G., and Air, G., eds., pp.69-79, E
A;Title: The haemagglutinin gene of influenza A virus: nucleotide sequence analysis of C
A;Reference number: A94441
A;Accession: A9445
A;Residues: 1-566 (SLE)
C;Superfamily: influenza virus hemagglutinin
C;Keywords: hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;11-16/Domain: signal sequence #status predicted <HAl>
F;346-566/Product: hemagglutinin HA2 #status predicted <HAl>
F;355,562,565/Binding site: palmitate (Cys) (covalent) #status predicted
Search completed: July 1, 2002, 06:28:12 Job time: 714 sec
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Matches 23; Conservative
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Query Match Best Local Similarity

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-i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIROLUMN CELL RECEPTORS AND FOR INITIATING INFECTION.

-i- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO (HAI AND HA2) LINKED BY A DISULFIDE BOND.

-i- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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P12583; Q84011;
01-OCT-1989 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor (Contains: Hemagglutinin
Hemagglutinin HA2 chain) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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MEDLINE-87265458; PubMed-2440178;
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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HEMA_IADH4 STANDARD; PRT; 550 AA.
P12585; Q84013; Q84014;
Q1-QCT-1989 (Rel. 12, Created)
Q1-QCT-1989 (Rel. 12, Last sequence update)
16-QCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin HAZ chain] (Fragment).
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PIR; C27813; HMIV33
InterPro; IPR001364; Hemagglutn
Pfam; PF00509; Hemagglutnin; 1.
ProDom; PD000225; Hemagglutn; 1.
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Influenza A virus (strain A/Duck/Hokkaido/7/82).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
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Viruses; ssRNA negative-strand viruses; Orthomyx
Influenza virus A and B group; Influenza A virus
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Y., Naeve C.W.,
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H3 influenza
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2.3e-07;
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RESULT 5
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P12886; Q84015; Q84016;
O1-CCT-1989 (Rel. 12, Created)
O1-APR-1990 (Rel. 14, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin HA1 chain;
Hemagglutinin HA2 chain] (Fragment).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                             MEDLINE-87265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Wel
"Antigenic and genetic conservation
                                                                                                                            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses; Influenza A virus.
                                                                                 SEQUENCE FROM
                                                                                                             NCBI_TaxID=11361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87265458; PubMed-2440178; Kida H., Kawaoka Y., Naeve C.W., Webster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Envelope protein; Hemagglutinin; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - 1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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Influenza
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SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.
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N-LINKED (GLCNAC. . . )
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Matches 23
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01-APR-1990 (Rel. 14, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hemagglutinin precursor (Contains. "Hemagglutinin precursor)
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MEDLINE=87265458; Pu
Kida H., Kawaoka Y.,
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by a
                                                                                                                                                           Influenza virus A
Influenza A virus
NCBI_TaxID=11362;
                                                                                                                                                                                     Influenza A virus (strain A/Duck/Hokkaido/9/85).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                                                                                                                                                                                        P12587; Q84017;
01-OCT-1989 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M16741; AAA43147.1;
PIR; E27813; HMIV21.
HSSP; P03437; 5HMG.
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-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAI (HAI AND HA2) LINKED BY A DISULFIDE BOND.
                                                                       Virology 159:109-119(1987).
                                                                                      ducks."
                                                                                                                                                                                                               Influenza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement
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                                                                                                 Antigenic and
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      FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE V
CELL RECEPTORS AND FOR INITIATING INFECTION.
SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO
(HAI AND HA2) LINKED BY A DISULFIDE BOND.
SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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23; Conserv
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                                                                                                           PubMed=2440178;
Y., Naeve C.W.,
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HEMAGGLUTININ HAZ CHAIN
N-LINKED (GLCNAC. . . ) (P)
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2.3e-07;
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influenza virus
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RESULT 7
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-87265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
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                                                         entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P12588; Q84018; Q89470;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin HA1 chain;
Hemagglutinin HA2 chain] (Fragment)
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-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                     Virology 159:109-119(1987).
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING CELL RECEPTORS AND FOR INITIATING INFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Influenza A virus (strain A/Duck/Hokkaido/10/85).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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between
                             EMBL; M16743; AAA43149.1;
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PIR; F27813; HMIV98.
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        G27813; HMIV15
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ProDom; PD000225; Hemagglutinin; Gl
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                                                                                                                                                                                                                                                                                                   of avian H3 influenza viruses to pigs in southern China, where the A/Hong Kong/68 (H3N2) strain emerged.";
J. Gen. Virol. 72:2007-2010(1991).
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS CELL RECEPTORS AND FOR INITIATING INFECTION.
-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAI (HAI AND HA2) LINKED BY A DISULFIDE BOND.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-91341491;
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(Rel. 32, Last sequence update)
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in precursor [Contains: Hemagglutinin HAl chain;
in HA2 chain] (Fragment).
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Pred. No. 2.3e-07;
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N-LINKED (GLCNAC. . .) (
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"Molecular evidence for a role of domestic ducks i
of avian H3 influenza viruses to pigs in southern
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J. Gen. Virol. 72:2007-2010(1991).
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATT
CELL RECEPTORS AND FOR INITIATING INFECTION.
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-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin HAI chain;
Hemagglutinin HA2 chain] (Fragment).
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                                                                            HEMAGGLUTININ HAI CHAIN.
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N-LINKED (GLCNAC. . .) (POT
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Score 134;
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2.3e-07;
                    DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00509; Hemagglutinin; ProDom; PD000225; Hemagglutn;
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                                                                                                                                                                                                                                                                                                                                    EMBL; D00930; BAA00770.1; HSSP; P03437; 5HMG.
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MEDLINE=91341491; Pubm
Yasuda J., Shortridge
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Influenza virus A a
Influenza A virus.
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin
Hemagglutinin HA2 chain] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Influenza A virus (strain A/Goose/Hong Kong/10/76).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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GLFGAIAGFIENGWEGMIDGWYG
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                                                            l Similarity 100 23; Conservative
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idge K.F., Shimizu Y.,
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                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                           Score 134;
Pred. No.
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HEMAGGLUTININ HA2 CHAIN.
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2.3e-07;
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RESULT 11 HEMA\_IAZH2

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                                            HEMA_IAZH3 STANDARD: PRT; 550 AA. P11134; Q84025; Q84026; Q1-JUL-1989 (Rel. 11, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hemagglutinin (Contains: Hemagglutinin HA1 chain; Chain) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VITOLOGY 162:160-166(1988).

- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VICELL RECEPTORS AND FOR INITIATING INFECTION.

- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO (HAI AND HA2) LINKED BY A DISULFIDE BOND.

- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Influenza A virus (strain A/Swine/Hong Kong/81/78). Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses; Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEMA_IAZH2 STANDARD; PRT; 550 AA.
p11133; Q84019; Q84020;
01-JUL-1989 (Rel. 11, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin (Contains: Hemagglutinin HAI chain; Hemagglutinin
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Influenza A virus (strain A/Swine/Hong Kong/126/82).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain] (Fragment).
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                                                                                                                                                                                                             GLEGATAGETENGWEGMIDGWYG 352
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l Similarity 100.0%;
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PD000225; Hemagglutn;
utinin; Envelope prote
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IPRO01364; Hemagglutn.
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nin gene of H3N2
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HEMAGGLUTININ HAZ CHAIN.
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                      0.
                                                                                                                                                                                                                                                                                    Score 134;
Pred. No.
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                                                                                                                                                                                                                                                                                                 Length 550;
                                                          Hemagglutinin
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SEQUENCE
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin Hemagglutinin HA2 chain].
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Virology 162:160-166(1988).
Virology 162:160-166(1988).

-i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATCELL RECEPTORS AND FOR INTIATING INFECTION.

-i- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS
(HAI AND HAZ) LINKED BY A DISULFIDE BOND.

(HAI AND HAZ) LINKED BY THE INFLUENZA HEMAGGLU
   WEDLINE-80254693; PubMed-7402351;
Verhoeyen M., Fang R., Min Jou W.,
Saman E., Fiers W.;
"Antigenic drift between the haemag
                                                                                                                                                                                   Influenza virus A and Influenza A virus. NCBI_TaxID=150147;
                                                                                                                                                                                                                                          Viruses; ssRNA negative-strand viruses; Orthomyxovi
Influenza virus A and B group; Influenza A viruses;
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P03437;
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CHAIN
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                                                                                                                           SEQUENCE FROM N.A.
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MEDLINE-88101364; PubMed-3336940;
Kida H., Shortridge K.F., Webster R.G.;
Kida H., Shortridge M.F., Webster R.G.;
                                                                                                                                                                                                                                                                                                            Influenza A virus (strain A/Aichi/2/68).
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NON_TER
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X-RAY CRYSTALLOGRAPHY (3.25 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (3.25 ANGSTROMS).

MEDLINE-98120975; PubMed-9461077;

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"Antigen distortion allows influenza virus to escape neutralization

Nat. Struct. Biol. 5:119-123(198).

-i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS

CELL RECEPTORS AND FOR INITIATING INFECTION.

-i- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAI

(HAI AND HAZ) LINKED BY A DISULETED BOND.

-i- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                           MEDLINE-94352388; PubMed-8072525; Bullough P.A., Hughson F.M., Skehel J.J., "Structure of influenza haemagglutinin at Nature 371:37-43(1994).
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    Wiley D.C.;
Wiley D.C.;
"The structure of a membrane
                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                     MEDLINE-90230310; PubMed-2329580; Weis W.I., Bruenger A.T., Skehel J.J., Wiley D.C. "Refinement of the influenza virus hemagglutinin annealing.";
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EMBO J. 9:17-24(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY.
MEDLINE-88232903; Pubm.
Weis W.I., Brown J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
MEDLINE-B1123029; PubMed-74649906;
Wilson I.A., Skehel J.J., Wiley D.C.;
"Structure of the haemagglutinin membrane virus at 3-A resolution.";
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[2]
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Nature 286:771-776(1980).
                                                     L; J02090; AAA431

L; V01085; CAA2422

L A93231; HMIVHA.

2 2HMG; 31-OCT-93

3 3HMG; 31-OCT-93

3 4HMG; 31-OCT-93

4 5HMG; 31-JAN-94

1 1HGD; 31-JAN-94
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J.H., Cusack S.C.,
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escape neutralization.";
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PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin;
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PDB; 2VIS; 29-APR-98.
PDB; 2VIU; 29-APR-98.
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PDB; 2VIU; 29-APR-98.
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                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ov send an email to license@isb-sib.ch).
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P26134;
Ol-MAY-1992 (Rel. 22, Created)
Ol-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin HA2 chain].
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                                                                                                                                                                                                        Influenza A virus (strain A/Duck/Alberta/78/76).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
NCBI_TaxID-11348;
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EMBL; M73771; -; NOT_ANNOTATED_CDS
                                                                                                                                            nonhuman hosts."
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SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.
SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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Pfam; PF00509; Hemagglutinin; 1. PRINTS; PR00329; HEMAGGLUTN12. ProDom; PD000225; Hemagglutn; 1. Envelope protein; Hemagglutinin; SIGNAL 1 16
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.P03442;
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16-OCT-2001 (Rel. 40, Last annotation updat
Hemagglutinin precursor [Contains: Hemagglu
Hemagglutinin HA2 chain].
                                                                                                                                                                                                                                                                                  Fang R., Min Jou W., Huylebroeck D., Devos R., Fiers W.;
"Complete structure of A/duck/Ukraine/63 influenza hemagglutinin
gene: animal virus as progenitor of human H3 Hong Kong 1968 influ
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Influenza A virus.
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                                                                                                                                                                                                   CELL RECEPTORS AND FOR INITIATING INFECTION.
SUBUNIT: HOMOTRIMER, EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
(HAI AND HA2) LINKED BY A DISULFIDE BOND.
SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                   EUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING
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Q1-MAR-2001 (TrEMBLrel. 16, L2
Q1-DEC-2001 (TrEMBLrel. 19, L2
HAEMAGGLUTININ PRECURSOR.
-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

EMBL; AJZ89703; CACL8525:1; -.

INTERPO; IPRO01364; Hemaggluth.
Pfam; PP00509; Hemaggluthii; 1.
PRINTS; PR00329; Hemaggluth; 1.
PRINTS; PR00329; Hemaggluth; 1.
PRINTS; PR00325; Hemaggluth; 1.
ENvelope protein; Glycoprotein; Hemagglutinin; Signal.
SIGNAL 1 16

POTENTIAL.
SEQUENCE 566 AA; 63356 MW; OBA681929300F72F CRC64;
                                                                                                                                                                                                   neuraminidase.".

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: HEMAGGLUTIMIN IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID-41857;
                                                                                                                                                                                                                                                                                  STRAIN-CLONE 7A (H3N2);
Mohsin M.A., Morris S.J.,
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                         Influenza A virus H3N2.
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
MEDLINE-95146951; PubMed-7844533;
Callan R.J., Early G., Kida H., Hinshaw V.S.;
Callan R.J., Early G., Kida H., Hinshaw V.S.;
"The appearance of H3 influenza viruses in seals.";
J. Gen. Virol. 76:199-203(1995).
J. Gen. Virol. 76:199-203(1995).
PUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

(HAI AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
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MEDLINE-9516951; PubMed-7844533;

MEDLINE-9516951; PubMed-7844533;

Callan R.J., Early G., Kida H., Hinshaw V.S.;

Callan R.J., Early G., Kida H., Hinshaw V.S.;

"The appearance of H3 influenza viruses in seals.";

J. Gen. Virol. 76:199-203(1995).

J. Gen. Virol. 76:199-703(1995).

GELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

J. SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HAZ) LINKED BY A DISCUFFIDE BOND (BY SIMILARITY).

J. SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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Q67125;
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                                                                                                                       STRAIN-A/SEAL/MA/3984/92;
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Probom; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein; Hemagglutinin,
Envelope protein; Glycoprotein; Hemagglutinin,
SEQUENCE 566 AA; 63456 MW; AE556302A9EEB99F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L31949; AAA64229.1; -. HSSP; P03437; 2VIU.
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                            Influenza A virus
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Influenza virus A and B group;
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EMBL; L32024; AAA64228.1; -.
HSSP; P03437; 2VIU
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
PRODOM; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein; Heiseguence 566 AA; 63441 MW; 590
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Q67132;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
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ProDom; PD000225; Hemagglutn; 1.
Probom; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein; HemaggluTinin.
CHAIN 1 344
HEMAGGLUTININ.
CHAIN 346 566
NEURAMINIDASE.
                                                                                                                                                                                                                                                (II) Carlile M.J., Collins J.F., Moseley B.E. B. (eds.);
SYMPOSIUM OF THE SCCIETY FOR GENERAL MICROBIOLOGY, pp.285-311,
Cambridge University Press, New York (1981).

-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

-!- SUBJUNT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAI
(HAI AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
                                                                                                                                                                                                             EMBL; M55059; AAA43239.1; -. HSSP; P03437; 1HGE.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-A/AICHI/2/68;
                                                                                                                                                                                                                                                                                                                                                                                                             Influenza A virus (strain A/Aichi/2/68).
Viruses; SSRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influ
NCBI_TaxID-150147;
                                                                                                               SEQUENCE
                                                                                                                                                                                   InterPro; IPRO01364; Hemagglutn. Pfam; PF00509; Hemagglutinin; 1.
                                                                                                                                                                                                                                      -! - SIMILARITY: BELONGS TO THE INFLUENZA
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TITLE THE MONOTRIMER BOLD (BY SIMILARITY).

CC (HAI AND HAZ); HEELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY).

CC 1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

CC (HAI ADA HAZ) LINKED BY A DISULFIDE BOND (BY SIMILARITY).

CR HSSP; PO3437; 1HGE.
                                                                                                                                                                                                                                                                                                RESULT
Q91MA7
    RRRR ROCCOCCOCC
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Best Local S
Matches 23
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01-DEC-2001
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                  STRAIN-A/HONG KONG/1/68(H3N2);
MEDLINE-21287244; PubMed-11371620;
                                       SEQUENCE FROM
STRAIN-A/HONG
                                                                                               Influenza A virus (A/Hong Kong/1/68(H3N2)).
Viruses; SSRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza NCBI_TaxID=108859;
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SIGNAL
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Sleigh M.J., Both G.W., Underwood P.A., Bender V.;
"Antigenic drift in the hemagglutinin of the Hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001364; Hemagglutn. Pfam; PF00509; Hemagglutinin; 1.
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antigenicity.";
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Both G.W., Sleigh
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01-DEC-2001
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HEMAGGLUTININ.
            STRAIN-A/SHOREBIRD/TAIWAN/31-4/99;
Lee M.S., Cheng P.C., Shien J.H., Cheng M.C., Lee
"Identification and subtyping of avian influenza
transcription-polymerase chain reaction.";
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                                                                                                                                        Viruses; ssRNA negative-strand Influenza virus A and B group; NCBI_TaxID=140665;
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Brown E.G., Liu H., Kit L.C., Baird S., Nesrallah M.;
"Pattern of mutation in the genome of influenza A virus on adaptation
to increased virulence in the mouse lung: Identification of functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. EMBL; AF348176; AAK51718.1; -. SEQUENCE 566 AA; 63387 MW;
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ProDom;
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Virulence of influenza virus for mice is associated with loss of oligosaccharide from the hemagalutinin molecule.";

Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

-- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINED BY TWO CHAINES.

-- (HAI AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
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01-NOV-1996 (TrEMBLrel. 01, Created)
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-I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
EMBL; AF311750; AAG33016.1; -.
INTETPRO. IFR001364; Hemagglutn.
PRINTS: PR00329; HEMAGGLUTN12.
PRODOR: PD000225; HEMAGGLUTN1; 1.
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01-NOV-1996 (TrEMBLrel. 01,
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HAEMAGGLUTININ (FRAGMENT).
                               STRAIN-A/PHILIPPINES/2/82 (H3N2);
Hartley C.A., Ward A.C., Anders E.M.;
"Virulence of influenza virus for mice is associated with
oligosaccharide from the hemagglutinin molecule.";
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                         Viruses; ssRNA negative-strand viruses; (Influenza virus A and B group; Influenza NCBI_TaxID=11320;
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-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HAZ) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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MEDLINE-97300854; PubMed-9155874;
Hartley C.A., Reading P.C., Ward A.C., Anders E.M.;
"Changes in the hemagglutinin molecule of influenza t virus associated with increased virulence for mice.";
Arch. Virol. 142:75-88(1997).
            SEQUENCE FROM N.A
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InterPro; IPR001364; Hemagglutn.
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-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).
-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAIL AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGITHTON.
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01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                    "Recent H3N2 swine influenza virus with haemagglutinin an nucleoprotein genes similar to 1975 human strains.";
J. Gen. Virol. 76:697-703(1995)
-i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMIL CELL RECEPTORS AND FOR INITIATING I
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SEQUENCE
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-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
EMBL: U07146: AAARTYBI 1 -
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                                                                                                                                                                                                                                                                                          EMBL; U07146; AAA85781.1; -. HSSP; P03437; 2VIU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bikour M.H., Frost E.H., Elazhary Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-A/SWINE/ANGE-GARDIEN/150/90(H3N2);
MEDLINE-95205091; PubMed-7897358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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Influenza virus A and B group;
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HSSP; P03437; 2VIU.
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InterPro; IPR001364; Hemagglutn.
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Pred. No. 6.9e
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Pred. No. 6.7e-08;
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Query Match
Best Local :
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01-NOV-1996 (TI
01-DEC-2001 (TI
HEMAGGLUTININ (
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Nature
[2]
                   STRAIN-A/FUKUOKA/C29/85 (H3N2);
MEDLINE-81030852; PubMed-7421990;
Gething M.-J., Bye J., Skehel J., Waterfield M.;
"cloning and dna sequence of double-stranded copie
genes from h2 and h3 strains elucidates antigenic
human influenza virus.";
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Influenza virus A and B group;
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EMBL; M65018; AAA43151.1;
HSSP; P03437; 2VIU.
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Submitted (XXX-1991) to
                                                                                      SEQUENCE FROM N.A.
                                                                                                          NCBI_TaxID-11320;
                                                                                                                                               Influenza
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ProDom; PD000225; Hemagglutn; 1.
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InterPro; IPR001364; Hemagglutn.
Location Hemagglutinin; 1.
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Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
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Pred. No. 7e-08;
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Best Local S
Matches 21
                                                                                                                                                        STRAIN-A/SICHUAN/2/87 (H3N2);

MEDLINE-93233219; PubMed-7682624;

Okuno Y., Isegawa Y., Sasao F., Ueda S.;

"A common neutralizing epitope conserved between the hemagglutinins of influenza a virus H1 and H2 strains.";

J. Virol. 67.2552-2558(1993).

-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INPECTION (BY SIMILARITY).

-I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAL AND HAZ) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
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067051;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gething M.-J., Bye J., Skehel J., Waterfield M.; "cloning and dna sequence of double-stranded copies of haemagylutinin genes from h2 and h3 strains elucidates antigenic shift and drift in human influenza virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001364; Hemagglutn. Pfam; PF00509; Hemagglutinin; 1. PRINTS; PR00329; HEMAGGLUTN12. ProDom; PD000225; Hemagglutn; 1.
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-!- SIMILARITY: BELLONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
EMBL; D13581; BAA02776.1; -.
HSSP; P03437; 1HTM.
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Okuno Y., Isegawa Y., Sasao F., Ueda S.;
"A common neutralizing epitope conserved between the hemagglutinins of influenza a virus H1 and H2 strains.";
J Virol. 67:2552-2558(1993)
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).
                                                                                EMBL; D13582;
HSAP; P03437;
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STRAIN-A/FUKUOKA/C29/85 (H3N2);
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
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STRAIN-A/SICHUAN/2/87 (H3N2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Influenza virus A and B group; Influenza A viruses.
NCBI_TaxID-11320;
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                                                                                                       SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY L; D13582; BAA02777.1; -.
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## ALIGNMENTS

RESULT AAB13784

AAB13784 standard; peptide; 44 AA

10-NOV-2000 (first entry)

Soluble tandem HA/ pK peptide conjugate.

Antigens modified by the covalent addition of a peptide that facilitates entry into antigen presenting cells, useful for compositions for immunizing against tumors and pathogens -WPI; 2000-442365/38. 14-DEC-1998; 14-DEC-1999; pk peptide; cytostatic; vaccine; cytotoxic T cell; CTL; immunotherapy; major histocompatibility complex class 1; MHC class 1; antigen; tumour; prostate; breast; multiple myeloma; HA peptide. 22-JUN-2000 W0200035949-A1 Unidentified. (DEND-) DENDREON CORP. Hakim I, 98US-0112324 99WO-US29724. Vidovic Ö

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The invention relates to a non-naturally occurring gene therapy vector, comprising an inner shell having a core complex containing a nucleic acid and at least one complex forming reagent. The vectors are stable having a nimproved outer steric layer that provides enhanced target specificity, in vivo and colloidal stability. The vectors are relatively homogeneous and comprise chemically defined species. The vectors demonstrate improved call entry and intracellular trafficking, permitting enhanced nucleic acid therapeutic activity such as gene expression. The present sequence is that of the peptide K14 Fuso, comprising a fusogenic peptide derived from influenza haemagglutinin and peptide K14, useful in the preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to compositions of modified soluble protein antigens capable of eliciting an enhanced in vivo cytotoxic T cell (CTL) response i.e. a major histocompatability complex (MHC) class I molecule response. The protein antigen is modified by the covalent addition of a peptide sequence which facilitate entry of the antigen into antigen presenting cells (APCs). The present sequence is one such peptide sequence which can be used to modify the soluble antigens. The present sequence is tandem HA/ pK peptide conjugate. The modified antigen composition may be used for immunising against, or treating a tumour e.g.
                                                                                                                                                                                                          Non-naturally occurring gene therapy vector useful for gene therapy, comprises an inner shell having a core complex containing a nucleic acid and at least one complex forming reagent -
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                                                                                                                               The present invention relates to compositions of modified soluble protein antigens capable of eliciting an enhanced in vivo cytotoxic T cell (CTL) response i.e. a major histocompatability complex (MHC) class I molecule response. The protein antigen is modified by the covalent addition of a peptide sequence which facilitate entry of the antigen into antigen presenting cells (APCs). The present sequence is one such peptide sequence which can be used to modify the soluble antigens. The present sequence is peptide HA. The modified antigen composition may be used for immunising against, or treating a tumour e.g. prostate and breast carcinoma or multiple myeloma, or pathogen in mammals.
                                                                                                           Sequence
                                                                                                                                                                                                                                                                  Claim 2; Page 26; 34pp; English.
                                                                                                                                                                                                                                                                                       Antigens modified by the covalent addition of a peptide that facilitates entry into antigen presenting cells, useful for compositions for immunizing against tumors and pathogens -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multiple myeloma
                                                                                                                                                                                                                                                                                                                                                                Vidovic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.0%;
90.0%;
                                                            100.0%;
                                                                      58.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΗA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for the invention
                                              0;
                                                         Score 143;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
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Pred. No. 1.1e-16;
24
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                                               Mismatches
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                                                         6.4e-
                                                                       DB 21;
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                                                                      Length
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                                              0;
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                                              Gaps
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RESULT ' 4
AAR2600
AC AAR260
AA
AAW34269
ID AAW3
XX AAW3
XX 14-M
XX 14-M
XX Synt
XW Virc
KW drug
XX Canc
XX Synt
XX Synt
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                           Virosome; vesicle; cationic lipid bilayer; viral fusion peptide; drug delivery system; membrane; gene therapy; diagnosis; treatme cancer; leukaemia; viral infection.
                              Synthetic
                                                                                                                                                                                  Synthetic lipid vesicle fusion peptide 1.
                                                                                                                                                                                                                                            14-MAY-1998
                                                                                                                                                                                                                                                                                                 AAW34269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAR26004-19 are influenza fusion peptides, derived from the influenza virus haemaggluthini gene which were used for the preparation of synthetic membrane vessicles. The arrangment of at least one, pref. three cystein residues at one end of these peptides has been found useful for the fusion activity, for the fusion of the liposome to the target cell membrane. The liposomes produced using these peptides can contain at least one active drug and can be used to target cells infected with cancer
                                                                                                                                                                                                                                                                                                                                                      AAW34269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 13pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drug-contg. phospholipid bi:layer vesicle with cell-specific markers on membrane - where markers have at least 90 per cent biological activity, used as pharmaceuticals against e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gluck R, Herrmann P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-270078/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NIKA-) NIKA HEALTH PROD LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemagglutinin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR26004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 143;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptides can contain at least one target cells infected with cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13;
7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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24 - NOV - 2000

NZ504444-A. Unidentified

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Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC Peptides AAW34269-W34284 represent novel lipid vesicles with positively CC charged lipid bilayer membranes composed of a cationic and/or CC polycationic lipid and at least one natural or synthetic viral fusion CC peptide integrated in, or covalently linked to, the membrane. Such CC peptides are used as drug delivery ystems, preferably for (non-)specific delivery of genetic material to target cells or tissues, CC particularly for diagnosis, treatment (especially antisense treatment) of cancer, leukaemia and viral infections in humans or animals. Genetic CC material is delivered, without infection, to resting or proliferating CC cells, in vitro or in vivo. When the genetic material is an antisense continuous lipid layer does not leak. The peptides do not need to fuse CC with, or destabilise, plasma membranes in order to enter the cytoplasm, CC since the fusion peptide ensures cell penetration by endocytosis (after Which fusion of the vesicle and endosomal membrane occurs). The genetic CC material thus has a greater chance of reaching the nucleus before it is cefficient than when using liposomes or conventional virosomes, so
                                                                                                               Cationic virosome; cytostatic; gene therapy; viral haemagglutinin; drug delivery; cancer;
                                                                                                     crosslinker
                                                                                                                                                            Cationic virosome crosslinker
                                                                                                                                                                                           14-MAY-2001
                                                                                                                                                                                                                          AAB70090;
                                                                                                                                                                                                                                                     AAB70090 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vesicle with cationic lipid bilayer that includes viral fusion peptide - used for delivery of genetic material to cells, especially for gene therapy of cancer, leukaemia and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-558673/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NIKA-) NIKA HEALTH PROD LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9741834-A1
                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               doses can be used,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                      58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waelti ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              avoiding possible toxicity associated with the
                                                                                                                                                                                                                                                       26
                                                                                                                                                                                                                                                                                                                                                                                                      Score 143; DB 18; Pred. No. 7e-11;
                                                                                                                                                                                                                                                                                                                                                                                        .0
                                                                                                                                                             #1 for
                                                                                                                                                                                                                                                       ⋧
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                          polypeptide binding
                                                                                                               lipid bilayer vesicle;
leukaemia; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 26;
                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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AAW299226
ID AAW2
XX AAW2
AC AAW2
DT 02-M
DE Memb
XX Infl
XX W097
PN W097
PN W097
PN 13-E
PR 13-E
PR 15-E
XX WPI;
XX WPI;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a crosslinker which is capable of linking to the surface of a novel cationic virosome and is capable of binding polypeptides. The cationic virosome is a lipid bilayer vesicle comprising a membrane with a net positive charge and contains 5-30 weight % based on total lipids, 1,3-dioleoylovy 2-(6-carboxy-spermyl)-propyl-amide (DOSPER), together with other lipids and at least one active fusogenic peptide. The fusogenic peptide is a viral haemagglutinin that causes the vesicle to be internalised by target cells through phagocytosis or endocytosis. The virosome is useful for delivering a desired drug or substance, preferably a nucleic acid, to target cells (resting or proliferating mammallan cells) such as cancer cells, leukaemic cells or virally infected cells in vitro, in diagnostic or medical applications and for the manufacture of medicament for carrying out non-infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipid bilayer vesicle, useful for delivering drugs to target cells such as cancer, leukemic, or virally infected cells, comprises viral glycoproteins in positively charged membrane -
                                                                                                                                                                                                                   Synthetic.
Influenza virus
                                          Kichler A,
                                                                                                   15-FEB-1996;
                                                                                                                                13-FEB-1997;
                                                                                                                                                             21-AUG-1997
                                                                                                                                                                                        W09730170-A1
                                                                                                                                                                                                                                                            Membrane active; acidic peptide; cationic lipid; transfection; gene therapy; tumour; vaccine; cytokine gene.
                                                                                                                                                                                                                                                                                                                                     02-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                  AAW29226
                                                                                                                                                                                                                                                                                                                                                                                           AAW29226 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-233042/24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                       (BOEH ) BOEHRINGER INGELHEIM INT GMBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cglfgaiagfiengwegmidgwyg
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                                                                                                                                                                                                                                                                                                       active acidic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 14; 41pp; English.
                                          Mechtler K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA:
                                                                                                   96DE-4005548.
                                                                                                                                97WO-EP00649.
                                                                                                                                                                                                                                                                                                                                                                                          peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein
                                                                                                                                                                                                                                                                                                       peptide INF6 from W09730170.
                                           Wagner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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A new composition has been developed for transfecting higher eukaryotic CC cells contains: (i) a complex of nucleic acid to be expressed plus a CC suboptimal concentration of one or more cationic lipids, and optionally CC at least one auxiliary lipid; and (ii) the new feature, at least one membrane-active, acidic peptide; where the ratio total positive CC charges: total negative charges in the composition is about 0-3, CC preferably 0-2. The present sequence represents a specifically claimed acidic peptide for use in the composition. The composition is used for CC transfection in vitro, in vivo or ex vivo, particularly for gene CC thrappy. A typical application is production of tumour vaccines from CC autologous cells transfected with a cytokine gene. The acidic peptide CC destabilises the endosomal membrane and significantly increases CC transfection efficiency, e.g. by as much as 1000 times, equivalent to that achieved with the optimal amount of cationic lipid. The acidic peptide also makes the transfection complex less sensitive to serum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition containing nucleic acid complexed with cationic lipid and a membrane-active, acidic peptide - used to increase efficiency of transfection by destabilising the endosomal membrane, especially useful for gene therapy
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 33; 63pp; German
   23 AA;
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Matches
                                           Query Match
Best Local
2 GLFGAIAGFIENGWEGMIDGWYG
                                    23;
                                            Similarity
                                  Conservative
                                           55.1%;
100.0%;
                                          Score 134; DB 18; Pred. No. 7.7e-10;
                                  0; Mismatches
                 24
                                                   Length 23;
                                  Indels
                                  0
                                  Gaps
                                  0
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В δ

AAR98016; AAR98016 standard; peptide; œ 25 ξ

Fusogenic peptide derived from HA-2 spike glycoprotein

12-NOV-1996

(first entry

Fusogenic peptide; spike glycoprotein; enveloped virus; vaccine; EMDPC; endosome membrane disruption promoting component; cationic polyamine; multifunctional molecular complex; foodstuff; herbicide; insecticide; plant growth regulator; miticide; rodenticide; fungicide; parasiticide; nematocide; immunisation; pathogen; therapy; autoimmune disease; hyperproliferating

Synthetic

WO9610038-A1

04-APR-1996

28-SEP-1995; 95WO-US12502

28-SEP-1994; 94US-0314060

(APOL-) APOLLON INC

Boutin RH;

WPI; 1996-200887/20

New complexes for nucleic acid transfer to target cells - comprising a nucleic acid compsn. and a cationic poly:amine with an endosome membrane disruption component.

Disclosure; Page 30; 138pp; English

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RESULT
AAR26005
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
The sequences given in AAR26004-19 are influenza fusion peptides, derived from the influenza virus haemagglutinin gene which were used for the preparation of synthetic membrane vessicles. The arrangment of at least one, pref. three cystein residues at one end of these peptides has been found useful for the fusion activity,
                                                                                                                                        Drug-contg. phospholipid bi:layer vesicle with cell-specific markers on membrane - where markers have at least 90 per cent biological activity, used as pharmaceuticals against e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transfer moiety comprising one or more cationic polyamine components bound to the nucleic acid composition. There are several different cationic polyamines that can be used in the complex, one of which contains one of these sequences linked via a bridging group to the main body of the cationic polyamine. The products can be used for delivering therapeutic agents, vaccines, foodstuffs, herbicides, plant growth regulators, insecticides, mittcides, rodenticides, fungicides, parasiticides or nematocides. They can also be used for immunising an individual against a pathogen or for treating an autoimmune disease or hyperproliferating disease. The complexes provide for a high level of transfection and expression of the nucleic acid molecules in target
                                                                                                 Disclosure;
                                                                                                                                                                                                               WPI; 1992-270078/33
                                                                                                                                                                                                                                            Gluck R,
                                                                                                                                                                                                                                                                                                        02-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences were used in a transfer moiety which makes up part of the multifunctional molecular complex of the invention. The multifunctional molecular complex is used for the transfer of a nucleic acid composition to a target cell, and comprises the nucleic acid composition and a
                                                                                                                                                                                                                                                                                                                                                                     12-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                  EP497997-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR98010-R98041 represent fusogenic peptides derived from spike glycoproteins of enveloped viruses. These fusogenic peptides act as endosome membrane disruption promoting components (EMDPCs). These
                                                                                                                                                                                                                                                                         (NIKA-)
                                                                                                                                                                                                                                                                                                                                      02-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemagglutinin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Influenza fusion peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR26005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR26005 standard; peptide;
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                                                                                                                                  AIDS
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                                                                                                                                                                                                                                                                         HEALTH PROD LTD
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                                                                                                                                                                                                                                                                                                                                      91EP-0101414
                                                                                                   2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cystein; liposome
                                                                                                13pp;
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                                                                                                                                                                                                                                            Klein
                                                                                                 English
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Pred. No. 8.5e-10;
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RESULT 1
AAW34270
                 CC Peptides AAW34269-W34284 represent novel lipid vesicles with positively CC charged lipid bilayer membranes composed of a cationic and/or polycationic lipid and at least one natural or synthetic viral fusion CC peptide integrated in, or covalently linked to, the membrane. Such CC peptides are used as drug delivery systems, preferably for (non-)specific delivery of genetic material to target cells or tissues, CC particularly for diagnosis, treatment (especially antisense treatment) of cancer, leukaemia and viral infections in humans or animals. Genetic CC material is delivered, without infection, to resting or proliferating CC cells, in vitro or in vivo. When the genetic material is an antisense CC with, or destabilise, plasma membranes in order to enter the cytoplasm, CC with or destabilise, plasma membranes in order to enter the cytoplasm, CC which fusion peptide ensures cell penetration by endocytosis (after CC which fusion of the vesicle and endosomal membrane occurs). The genetic CC material thus has a greater chance of reaching the nucleus before it is degraded or expelled. Transfer of the material is 1000-20000 times more centred when using liposomes or conventional virosomes, so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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Best Local S
Matches 23
           smaller doses can be used,
                                                                                                                                                                                                                                                                                                                                                    Vesicle with cationic lipid bilayer that includes viral fusion peptide - used for delivery of genetic material to cells, espender gene therapy of cancer, leukaemia and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9741834-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for the fusion of the liposome to the target cell membrane. The liposomes produced using these peptides can contain at least one active drug and can be used to target cells infected with cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                Glueck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             delivery system; membrane;
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23; Conservative
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                                                                                                                                                                                                                                                                                                                        Page 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide;
                                                                                                                                                                                                                                                                                                                        52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                              Waelti ER
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a crosslinker which is capable of linking to the surface of a novel cationic virosome and is capable of binding polypeptides. The cationic virosome is a lipid bilayer vesicle comprising a membrane with a net positive charge and contains 5-30 weight 8 based on total lipids, 1,3-dioleoyloxy-2-(6-carboxy-spermyl)-propyl-amide (DOSPER), together with other lipids and at least one active fusogenic peptide. The fusogenic peptide is a viral haemaggluthnin that causes the vesicle to be internalised by target cells through phagocytosis or substance, preferably a nucleic acid, to target cells (resting or substance, preferably a nucleic acid, to target cells, leukaemic cells or viral the manufacture of maddical applications and active comment of modifications of modification of modification of modification of modifications of modification of modifications of modifi
                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipid bilayer vesicle, useful for delivering drugs to target cells such as cancer, leukemic, or virally infected cells, comprises viral glycoproteins in positively charged membrane -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-233042/24
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23; Conser
                                                                                                                                                                                                                                                                                                                                                                             the manufacture of medicament for
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in; drug delivery; cancer; leukaemia; viral infection;
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                                                               Score 134; DB 10;
; Pred. No. 8.8e-10;
                                                                                                                                                                                                                                                                                                                                                                     carrying out non-infectious
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Conservative

55.1%; Score 134; DB 17; 100.0%; Pred. No. 9.5e-10; tive 0; Mismatches 0;

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Gaps

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RESULT
AAR98024
                                              transfer molety comprising one or more cationic polyamine components bound to the nucleic acid composition. There are several different cationic polyamines that can be used in the complex, one of which contains one of these sequences linked via a bridging group to the main body of the cationic polyamine. The products can be used for delivering therapeutic agents, vaccines, froodstuffs, herbicides, plant growth regulators, insecticides, mittcides, rodenticides, fungicides, parastiticides or nematocides. They can also be used for immunising an individual against a pathogen or for transfection and expression of the nucleic acid molecules in target
                                                                                                                                                                                                                                         AAR98010-R98041 represent fusogenic peptides derived from spike glycoproteins of enveloped viruses. These fusogenic peptides act as endosome membrane disruption promoting components (EMDPCs). These sequences were used in a transfer moiety which makes up part of the multifunctional molecular complex of the invention. The multifunctional molecular complex of the invention. The multifunctional molecular complex is used for the transfer of a nucleic acid composition and a target cell, and comprises the nucleic acid composition and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New complexes for nucleic acid transfer to target cells - comprising a nucleic acid compsn. and a cationic poly:amine with an endosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endosome membrane disruption promoting component; cationic polyamine; multifunctional molecular complex; foodstuff; herbicide; insecticide; plant growth regulator; miticide; rodenticide; fungicide; parasiticide
Sequence
                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                membrane disruption
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boutin RH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (APOL-) APOLLON INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusogenic peptide; spike glycoprotein; enveloped virus; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusogenic peptide derived from HA-2 X:31 spike glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1996
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28
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                                                                                                                                                                                                                                                                                                                                                                                               English.
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                       ABB01088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interleukin, interferon, colony stimulating factor, hormone or angiogenic factor. The peptides of the invention can be used for inhibiting viral infection and can be used in anti-fursion and infection and can be used in anti-fursion treatments. Sequences AAY88651-Y90055 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends
                                                                           ABB01088 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A new hybrid polypeptide with enhanced comprises enhancer sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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23; Conserv
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                                                                        Peptide;
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100.0%;
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Best Local
       Human immunodeficiency virus; HIV; respiratory syncytial virus; virucide; heptad repeat region; transmembrane protein; gp41; HR
                                              Viral core polypeptide, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107. correspond to amino acids 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-ILAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in
                                                                          03-JAN-2002
                                                                                                    ABB02537;
                                                                                                                        ABB02537 standard; Peptide;
                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                   the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection
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Search completed: July 1, 2002, 06:19:25
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                                                                                                                                                                                                                                                                           The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP165. Garcespond to amino acids 638-673 (heptad repeat region HR1) respectively, of HIV-ILAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytlal virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the percent region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus infection - \,
                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 448; 587pp; English.
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! FINDPATT	TERNS on gen	FINDPATTERNS on genesegp: * allowing 0 mismatches
	AAW45801	ck: 9500 len: 39 ! Aaw45801 One chain of a bombesin dimer. 6/1
1	<b>1</b>	C(R,K){20} CKKKKKKKKKKKKKKKK XGGGQ
	AAB13780	ck: 7317 len: 21   Aab13780 Soluble peptide antigen pK. 11/200
1	1:	C(R,K){20} C(K){20}
	AAU18238	ck: 5509 len: 58 ! Aaul8238 Novel human DNA-binding protein #8
4	35: KFYFV	C(R,K){20} C(K){20} S5: KFYFV CKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
	AA003766	ck: 8808 len: 81 ! Aao03766 Human polypeptide SEQ ID NO 17658.
ц	48: LTTTA	C(R,K){20} C(K){20} 48: LTTTA CKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
	AA011210	ck: 863 len: 70 ! Aaol1210 Human polypeptide SEQ ID NO 25102.
ч	30: IDLCL	C(R,K)(20) C(K)(20) CKKKKKKKKKKKKKKKK KKKKK
Databases searched: EMBL, Releas	searched: BL, Release	es searched: EMBL, Release 7.0, Released on 28Apr2002, Formatted on 2May2002
Total finds: Total length: Total sequences: CPU time:		114,001,827 766,495 07:03.10

D# 6

pk peptide; cytostatic; vaccine; cytotoxic T cell; CTL; immunotherapy; major histocompatibility complex class 1; MHC class 1; antigen; tumour; prostate; breast; multiple myeloma.

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therapy vectors, allowing these to be endocytosed by GPCR-expressing cells. They can also be used e.g. to treat hypertension (angiotensin-based LD); to increase levels of luteliaising hormone (LH), using LD derived from LH-releasing hormone, or to promote skin tranning (LD based on alpha -melanocyte-stimulating hormone, MSH). The bivalent agonists are administered orally, by injection or topically. Typical doses for skin tanning are 1-4000 (especially 30-100) mu mole/kg systemically or containing are 1-4000 (especially 30-100) mu mole/kg systemically or containing on 1-10 (especially 1) mM. Where both LD are agonists, the bivalent agonist ligands, and where both LD are agonists, the bivalent agonist ligands, and where at least 1 is an antagonist the effect is stimulatory. The bivalent agonists are active at lower concentrations than known agonists so should avoid toxicity problems.
                                                                                                                                                                                                                                               bivalent agonists comprise: (a) two ligand domains (LD), individually agonists or antagonists for GPCR, spaced 40-250 Angstrom apart, and (b) a molecular backbone (MB) covalently bound to LD. The bivalent agonists are useful in human or veterinary medicine as carriers for drugs or gene
                                                                                                                                                                                                                                                                                                               This sequence represents one of two identical chains disulphide bonded to form a bombesin dimer. The invention relates to bivalent agonists, with affinity for at least 1 protein coupled receptor (GPCR). The
                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                          Bivalent agonist of G-protein coupled receptors containing two ligand domains - bonded to molecular backbone, for treatment of hypotension, promotion of skin tanning etc., also for delivering drugs and gene therapy vectors to selected cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carrithers MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-melanocyte stimulating hormone; alpha-MSH; receptor agonist; alpha-MSH-ANT; bombesin; dimer; bivalent agonist; disulphide bond;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _SEQUENCE 1.0
AAW45801 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                            Page 48; 71pp;
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39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US12911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "This residue is disulphide bonded to the corresponding Cys residue of an identica to form a dimer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Epsilon-aminohexanoic acid"
                                                                                                                                                                                                                                                                                                                                                                                              English.
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Claim 2;

Page 26; 34pp;

English.

Antigens modified by the covalent addition of a peptide that facilitates entry into antigen presenting cells, useful for compositions for immunizing against tumors and pathogens -

14-DEC-1999;

14-DEC-1998;

98US-0112324 99WO-US29724

(DEND-) DENDREON CORP

Unidentified.

10-NOV-2000

(first entry)

AAB13780;

Soluble peptide antigen pK

WO200035949-A1

Laus

Hakim I,

Vidovic

D;

WPI; 2000-442365/38

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WO200155162-A1
                                        cytostatic.
                                                         autoimmune disorder; rheumatic disease;
                                            immunomodulatory; anti-HIV;
                                                    intectious
                                                  disease; neurological disorder; gene therapy;
                                                       genetic abnormality;
```

chromatin organisation modifier; y-box binding protein; DNA organisation; gene transcription; malignant disease

Human; DNA-binding protein; histone; chromo domain protein;

Novel human DNA-binding protein #85.

21-NOV-2001 AAU18238;

(first entry)

I ! AA\_SEQUENCE 1.0
ID AAU18238 standard;

Protein;

58

CKKKKKKKKK KKKKKKKKKK

AAB13780

Length:

21

July 1, 2002 14:50

Type: ס

Check: 7317

21

A.

The present invention relates to compositions of modified soluble protein antigens capable of eliciting an enhanced in vivo cytotoxic T cell (CTL) response i.e. a major histocompatability complex (MHC) class I molecule response. The protein antigen is modified by the covalent addition of a peptide sequence which facilitate entry of the antigen into antigen presenting cells (APCs). The present sequence is one such peptide sequence which can be used to modify the soluble antigens. The present sequence is peptide by. The modified antigen composition may be used for immunising against, or treating a tumour e.g. prostate and breast carcinoma or multiple myeloma, or pathogen in mammals.

!!AA\_SEQUENCE 1.0
ID AAB13780 standard;

peptide;

AAW45801 Length: 39

July 1,

2002 14:50

Type: P

Check:

KKKKKKKKK KXGGGQQRLG NQWAVGHLM

17-JAN-2001;

2001WO-US01305

N

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29-SEP-2000
02-OCT 2000
02-OCT 2000
02-OCT 2000
02-OCT 2000
03-OCT 2000
03-NOV 2000
03-NOV
       WPI; 2001-465557/50
N-PSDB; AAS29114.
                                                      Rosen
                                                    CA,
                                                                                  HUMAN
                                                    Barash
                                                                                                           2000US-0237039
2000US-0237039
2000US-0237039
2000US-0237040
2000US-0237040
2000US-0241785
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2000US-0241808
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2000US-0246532
2000US-0246532
2000US-0249211
2000US-0251856
2000US-0251856
2000US-0251989
2000US-0251989
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2000US-0236802.
2000US-0237037.
                                                                                GENOME
                                                    SC
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                                                    Ruben
                                                    MS
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31-JAN-2000
24-FEB 2000
24-FEB 2000
24-FEB 2000
27-MAR-2000
28-JUN-2000
28-JUN-2000
29-JUN-2000
20-JUN-2000
21-JUL-2000
21-AUG-2000
21-SEP-2000
22-SEP-2000
23-SEP-2000
24-SEP-2000
25-SEP-2000
27-SEP-2000

2000US-017905
2000US-0184664
2000US-0184664
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2000US-019974
2000US-0199076
2000US-0199123
2000US-0121647
2000US-0121647
2000US-0121647
2000US-0121647
2000US-0121647
2000US-0121647
2000US-0121647
2000US-01217496
2000US-012511
2000US-0125214
2000US-0125214
2000US-0125266
2000US-0125276
2000US-012576
2000US-0

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!!AA_SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                              AAU18238 Length:
 The invention relates
                 Claim 20; SEQ ID NO 17658; 1399pp + Sequence Listing;
                                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                             WPI; 2001-514838/56.
                                                                     N-PSDB; AAI83697.
                                                                                                                               28-FEB-2000;
18-MAY-2000;
                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 17658
                                           diagnosing and treating
                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                        26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                        07-SEP-2001
                                                                                                                                                                                         WO200164835-A2
                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                     06-NOV-2001
                                                                                                                                                                                                                                                                                                      AA003766;
                                                                                                                                                                                                                                                                                                                     AAO03766 standard;
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                   Solated nucleic acids and
                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                               TYLECEHNSL VNSKCLTVVL SRCISVCLNK FYFVCKKKKK KKKKKKKKKKKK
                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                58
                                                                                                                              2000US-0515126.
2000US-0577409.
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                             Drmanac
                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                               July 1,
  to
                                         and polypeptides, useful for preventing e.g. leukaemia, inflammation and immun
human polynucleotides (AAI79941-AAI93841)
                                                                                             RT
                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                               2002 14:50
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                                                                                                                                                                                                                                                                                                                                                                              Type: P
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                 English
and
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cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, inmunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                 the encoded proteins (AAO00010-AAO13910) that exhibit activity
                                                                                                                                        intlammation
                                                                                                                                                                                                                                                                                                                                                                                                 elating to
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Sequence 81

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GLNQTQLRKI LAYSSITHIG

XIIAVLPYNP NITILNLTIY IILTTTACKK

organisation and/or gene transcription. The sequences of the invention are useful in screening assays to identify antagonists and/or agonists that may enhance or block activities mediated by DNA-binding proteins. Blockers of DNA-binding proteins may be useful in treating disorders such as malignant diseases (e.g. cancer), autoimmune disorders (e.g. diabetes mellitus), rheumatic diseases (e.g. rheumatoid arthritis), genetic abnormalities (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological disorders (e.g. Alzheimer's disease). The polynucleotide sequences of the invention may also be used in gene therapy. AAU18154-AAU18281 represent novel DNA-binding

at ftp.wipo.int/pub/published\_pct\_sequences.

The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from WIPO

specification,

proteins

The present invention relates to the isolation of novel DNA-binding proceins, and cDNA (AAS29030-AAS29157) and genomic sequences encoding proteins. DNA-binding proteins such as histones, chromo (chromatin organisation modifier) domain proteins, and Y-box binding proteins may contribute to diseases resulting from aberrant DNA proteins may contribute to diseases resulting from aberrant DNA

Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -

Claim 11; SEQ ID No 223; 561pp; English.

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AA003766
 Length: 81
 July 1,
 2002 14:50
Type: P
 Check: 8808
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51 KKKKKKKKK KKKKKKKKKK KKKKKKGGGG ×

!!AA\_SEQUENCE 1.0 Human polypeptide SEQ ID NO 06-NOV-2001 (first entry) AA011210; AAO11210 standard; Protein; 70 25102

Human; cytokine; cell proliferation; cell different vaccine; peptide therapy; stem cell growth factor; tissue growth factor; immunomodulatory; cancer; le nervous system disorders; arthritis; inflammation. cell differentiation; gene therapy; pr; haematopoiesis; leukaemia;

Homo sapiens.

WO200164835-A2

07-SEP-2001.

26-FEB-2001; 2001WO-US04927

28-FEB-2000; 18-MAY-2000; 2000US-0515126 2000US-0577409

(HYSE-) HYSEQ INC

Tang Liu C, Drmanac 刄

N-PSDB; 2001-514838/56. DB; AAI91141.

Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun 1mmune

Claim 20; SEQ Į NO 25102; 1399pp + Sequence Listing; English.

cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and Note: The sequence data for this patent did not form specification, but was obtained in electronic format The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to nflammation directly part of the printed from

CC at ftp.wipo.int/pu xx SQ . Sequence 70 AA; at ftp.wipo.int/pub/published\_pct\_sequences.

AAO11210 Length: 70 July 1, 2002 14:50 Type: P Check: 863 ..

1 YYIHRTTVFM CMNXGLKDNV DKXTIDLCLC KKKKKKKKKK KKKKKKKKKK

51 KKKKKKKKKK KKKKPQGGGA

GENESEDP2001:AA001766 Ck: 8808 len: 81 finds: 1 i Aac03766 Human polypeptide SE GENESEDP2001:AA011210 ck: 863 len: 70 finds: 1 i Aa011210 Human polypeptide SE N.End of List  Databases searched:  PRBL, Released 7.0, Released on 28Apr2002, Formatted on 2May2002  Prot1 finds: 5  Total length: 114.003.827  Total sequence: 09:53.67  CPU time: 09:53.67	I SEQUENCE_LIST 1.0   I FINDPATTERNS on geneseqp:* all   1 C(R,K){20}   CENESEQP1990S:AAW45801	owing len: len:	0 mismatches July 39 finds: 1 21 finds: 1 58 finds: 1	1, 2002 14:38 ! Aaw45801 One chain of a bomb ! Aab13780 Soluble peptide anti
7.0, Released on 28Apr2002, Formatted on 2May2002  5 114,001,827 766,495 09:53.67	<u>ç</u> <u>ç</u>			Aao03766 Human polypeptide Aao11210 Human polypeptide
ed: 5 114,001,827 766,495 09:53.67				1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	7.0,			
		7 61 7 61		

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I C(R,K){20}

Databases searched:
NBRF, Release 71.0, Released on 15Feb2002, Formatted on 19Feb2002

Total finds:
Total length:
Total sequences:
283,138
CPU time:
04:30.92
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Databases searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (R,K)(20)
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                                                                                                                                                                                                                                                                                 (R,K)[20]
55: RRTRR KRRKRRKRRKRRKRRKR SPRKR
                                                                                                                                                                                                                                                                                                                                                                                                                                           (R,K)[20]
54: KRRTR RKRRKRRKRRKRRKRRK RSPRK
                                                                                                                                                                                                                                                                                                                                                                              T46395 ck: 7330 len: 380 ! hypothetical protein DKFZp434I1120.1 - hum
                                                                                                                           I52523 ck: 8048 len: 215 ! nucleoporin p62 homolog - rat (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S58321 ck: 1384 len: 126 ! probable membrane protein YOR309c - yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T49173 ck: 4143 len: 517 / hypothetical protein T20N10.250 - Arabidops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       July 1, 2002 06:48 ..
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NBRF, Release 71.0, Released on 15Feb2002, Formatted on 19Feb2002

Total finds: 17
Total length: 96,089,334
Total sequences: 283,138
CPU time: 09:02.03

t # Be

		Total finds: Total length: Total sequences: CPU time:	Databases searched: NBRF, Release	\\End of list	PIR2:152523	PIR2:T46395	PIR2:S58321	PIR2:T49173	1 (R,K){20}	!!SEQUENCE_LIST 1.0
•		17 96,089,334 283,138 08:41.42	71.0,		ck: 8048	ck: 7330	ck: 1384	ck: 4143		<pre>:* allowing 0 mismatches</pre>
		2847	Released		len:	len:	len:	len:		9 O m
			9		215	380	126	517		ismatch
			15Feb2002,		finds:	finds:	finds:	finds:		es
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			Formatted on :		! nucleop	t hypothetical	! probab	! hypothe	, 2002 14:57	
			19Feb2002		nucleoporin p62	etical p	probable membrane	etical p	1:57	
			)2		homo.	protein	ane pro	rotein		
					og - rat	DKFZp434I	protein YOR3	hypothetical protein T20N10.25		

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A; Molecule type: DNA
A; Residues: 1-126 <PEA>
A; Residues: 1-126 <PEA>
A; Cross-references: EMBL: X90565; NID: g940836; PID: g940840
R; Pearson, B.M.; Hernando, Y.; Kalogeropoulos, A.; Schweissubmitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          !!AA_SEQUENCE 1.0
P1;T49173 - hypothetical protein T20N10.250 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 08-Dec-2000
C;Accession: T49173
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.; Quetler, F.; Salanoubat, M.
Yeast 12, 1021-1031, 1996
A;Title: Sequencing of a 35.71 kb DNA segment on the right arm of chromosome XV reveals regions of similarity to chromosomes I and A;Reference number: S71986; MUID:97051589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P1;S58321 - probable membrane protein YOR309c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein 06105
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1996 #sequence_revision
C;Accession: S58321; S67215; S71989
R;Pearson, B.M.; Hernando, Y.; Wolf, S.S.; Kalogeropoulos, A.; Schweizer, M. submitted to the EMBL Data Library, August 1995
                                                                                                                                  A; Experimental source: strain S288CR; Pearson, B.M.; Hernando, Y.; Payn
                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-126 < PEW>
                                                                                                                                                                                                                                                                                             A; Reference number: S67213
A; Accession: S67215
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A; Accession: S58321
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A:Introns: 312/3; 359/3; 444/3
C:Superfamily: Arabidopsis thaliana hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: ATSP:T20N10.250
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A;Residues: 1-517 <DAN>
A;Coss-references: EMBL:AL353032; GSPDB:GN00061; ATSP:T20N10.250
A;Experimental source: cultivar Columbia; BAC clone T20N10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               !!AA_SEQUENCE 1.0
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A;Accession. minima
                                                                                                             Schweizer,
                                                                                                                                                                                                       Cross-references: EMBL:Z75217; NID:g1420680; PID:e252431; PID:g1420681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501
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                                                                                                                             J.; Wolf, S.S.; Kalogeropoulos, A.
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                             yeast
XIII.
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C:Accession: 1525/23
R:Wang, Z.O.; Akmal, K.M.; Kim, K.H.
Biol. Reprod. 51, 1022-1030, 1994
A:Title: An unusual nucleoporin related messenger ribonucleic in the germ cells of rat testis.
                                                                                            A; Reference number: I52523;
A; Accession: I52523
                                                                                                                                                                                                                                                                        F1; I52523 - nucleoporin p62 homolog - rat (fragment) C; Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     !!AA_SEQUENCE 1.0

F1;T46395 - hypothetical protein DKFZp434II120.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C;Accession: T46395
A;Cross-references: GB:S75997; NID:g913245; PIDN:AAB33384.1; PID:g913246
                            A; Residues: 1-215 < RES>
                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                     C;Date: 27-Feb-1997 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: adult testis; clone DKFZp43411120 C; Genetics: A; Note: DKFZp43411120.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the Protein Sequence Database, January A;Reference number: Z23031
A;Accession: T46395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Map position: 15R
C;Keywords: transmembrane protein
F;3-19/Domain: transmembrane #status predicted
F;107-123/Domain: transmembrane #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-126 <PEF>
A;Cross-references: EMBL:X90565; NID:9940836;
A;Note: the nucleotide sequence was submitted
                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                               !!AA_SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: AL137556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-380 < AAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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A;Status: nucleic acid sequence not shown; translation
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                                                                                                                                                                                                                                                 27-Feb-1997 #text_change
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152523 Length: 215 July 1, 2002 15:06 Type: P Check: 8048 ...
1 SGGRATSSCD EDCLSSSLPF SLSGPVKQDC EFLEKKKKK KKKKKKKKK
51 KKKKKKTGDN AKSVSRQYSL KVTKLEHEAE QAKVELDFIL SQQKELEDLL
101 SPLEESVKEQ SGTIYLQHAD EEREKTYKLA ENIDAQLKRM AQDLKDIIEH
151 LNMAGGPADT SDPLQQICKI LNAHMDSLQW VDQSSALLQR RVEEASRVCE
201 SRRKEQERSL RIAFD

! FINDPATTERNS on swp: \* allowing 0 mismatches

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1 (R,K)[20]
80: KKKKK KKKKKKKKKKKKKKKKK KKKEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9HC48
                                Q9H6Q7
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                                                                                                                                                                                                                                                                                                                               ck: 7602
                                ck: 3351
                                len: 720
                                                                                      len: 667
                                                                                                                                                                                                                                                                                                                                                                                                                                    len: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! Q12444 saccharomyces cerevisiae (baker's
                                                                                  1 Q9hc48 homo sapiens (human). ctcl tumor an
                            ! Q9h6q7 homo sapiens (human). cdna: flj2197
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Q9p529 neurospora crassa. hypothetical 15
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(K)[20]
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                                                                                                                                                                  (R,K)(20)
(K)(20)
                                                                                                                                                                                len: 168
                 ! Q9nt34 homo sapiens (human). hypothetica
                                                                                                                                                                               ! Q9h5v6 homo sapiens (human). cdna: flj22
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356: LLLQK KKKKKKKKKKKKKKKKKKKK KKKKK

(K) [20]

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(K){20}
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Q9LGZ9 ck: 6094 len: 260 ! Q9lgz9 arabidopsis thaliana (mouse-ear cres
                                                                                                                                      Q9LxR2 ck: 4143 len: 517 ! Q91xr2 arabidopsis thaliana (mouse-ear cres
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Submitted (AUG-1995) to the EN
EMBL; 275217; CAA99629.1; -.
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SGD; S0005836; YOR309C.
SEQUENCE 126 AA; 16294 MW;
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Submitted
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                                                                                                                       Hypothetical SEQUENCE 12
                                                                                                                                           German Neurospora genome project; Submitted (OCT-2001) to the EMBL/EMBL; AL356815; CAB92638.2; -.
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SChulte U., Aign V.; Hoheisel J., Brandt P., E
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                  Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID-5141;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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HYPOTHETICAL 15.2 KDA PROTEIN.
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Pearson B.M., Hernando

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SMART; SM00228; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
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O9H6Q7;
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CDNA: FLJ21979 FIS, CLONE HEP06065 (FRAGMENT).
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CTCL TUMOR ANTIGEN SE2-5 (FRAGMENT).
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"NEDO human cDNA sequencing project.";
"Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK025632; BAB15196.1; -.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA: FLJ22976 FIS, CLONE KAT11222 (FRAGMENT).
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                  Tashiro H.,
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Submitted (SEP-2001) to the
EMBL; AB071085; BAB64479.1;
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=TESTIS;
Hashimoto K., Osada N., Hida M.,
Terao K., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 61.4 KDA PROTEIN (FRAGMENT).
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 42.7 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ottenwaelder B., Obermaier B., Submitted (JAN-2000) to the EMEMBL; AL137556; CAB70810.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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  Q9LGZ9 PRELIMINARY;
Q9LGZ9;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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Submitted (APR-2000) to the
EMBL; AL353032; CAB88307.1;
InterPro; IPR001810; F-box.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
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D'Angelo M., Vezzi A.,
Rudd S., Lemcke K., May
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01-0CT-2000 (TrEMBLrel. 15, La
01-0CT-2001 (TrEMBLrel. 18, La
19-0CT-2001 (TrEMBLrel. 18, La
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01-NOV-1996
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129 AA;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MICROVASCULAR ENDOTHELIAL DIFFERENTIATION PROTEIN 2.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Pfam; PF00069; pkinase; 1.
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Proels F., Loser B., Marx M
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'Differential expression of osteopontin,
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TISSUE*EPIDIDYMIS;
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NUCLEOPORIN P62 HOMOLOG PROTEIN (FRAGMENT).
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Rattus.
NCBI\_TaxID=10118;
[1]
SEQUENCE FROM N.A.
MEDLINE=95151924; PubMed=7849178;
Wang 2.Q., Akmal K.M., Kim K.H.;
"An unusual nucleoporin-related messenger ribonucleic acid is present in the germ cells of rat testis.";
Biol. Reprod. 51:1022-1030(1994).
EMBL; S75997; AAB33384.1; -.
POOTIN.
NON\_TER 1 1
SEQUENCE 215 AA; 24593 MW; 098251C97A8FBD88 CRC64;
SEQUENCE 215 AA; 24593 MW; 098251C97A8FBD88 CRC64;

1 SGGRATSSCD EDCLSSSLPF SLSGPVKQDC EFLEKKKKK KKKKKKKKKK

51 KKKKKKTGDN AKSVSRQYSL KVTKLEHEAE QAKVELDFIL SQQKELEDLL
101 SPLEESVKEQ SGTIYLQHAD EEREKTYKLA ENIDAQLKRM AQDLKDIIEH
151 LNMAGGPADT SDPLQQICKI LNAHMDSLQW VDQSSALLQR RVEEASRVCE
201 SRRKEQERSL RIAFD

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! FINDPATTERNS on geneseqp: * allowing 0 mismatches
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                                                          AAP61082 ck: 7915 len: 898 ! Aap61082 Complete translation of plasmid pA
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AAW38840 ck: 2989 len: 29

! Aaw38840 Delivery peptide used in peptid

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AAW38842 ck: 7590 len: 31
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                                                                                                      ! Aaw38842 Delivery peptide used in peptide
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AAW38878 ck: 2949 len: 24
                                                        AAW38843 ck: 3
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K KKKKKKKKKKKKKKKKKKKK VTK
                                                                                                                                                                                                                 ck: 1129 len: 23
                (R,K){20}
KKKKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                  len: 32
                                      ! Aaw38878 Delivery peptide used in pepti
                                                                                                                                                                                                                                                        ! Aaw38843 Delivery peptide used in pepti
                                                                                                                                                                                                                                                                                               ! Aaw38877 Delivery peptide used in pepti
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AAW38844 ck: 2491 len: 33

! Aaw38844 Delivery peptide used in pepti

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AAW38845 ck: 5054 len:
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                                                                                                                                                                                              AAW38879 ck: 4844 len: 25
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KK KKKKKKKKKKKKKKKKKKK VTK
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K KKKKKKKKKKKKKKKKKKKK KKKK
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KKKKKKKKKKKKKKKKKKKK KKKKK
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AAW38846 ck: 7692 len: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                  (K){20}
                       AAW38880 ck: 6814 len: 26
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10: KKKKK KKKKKKKKKKKKKKKKKKK KKKXK
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KKK KKKKKKKKKKKKKKKKKKK VTK
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KK KKKKKKKKKKKKKKKKKKK KVTK
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K KKKKKKKKKKKKKKKKKKKK KKYTK
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(K){20}
KKKKKKKKKKKKKKKKKKKKKKKKKKKKK
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                                                                                                                                                                                                                                                                                                                                                                                ! Aaw38880 Delivery peptide used in peptid
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! Aaw38834  KXK  XK  ! Aaw38835  ! Aaw38836  ! Aaw38837  ! Aaw38837  ! Aaw38837  ! Aaw38837  ! KKKK	AAW38833 ck: 9248 len: 22 (R,K)[20] (K)[20] (K)[20] KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK			XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX			× ^	*	*	83										
! Aaw38834  KXK  XK  ! Aaw38835  ! Aaw38836  ! Aaw38837  ! Aaw38837  ! Aaw38837  ! KKKK  KKKK  KKKK  KKKK  KKKK  KKKK  KKKK	ck: 9248 len: 22 (R,K)[20] (K)[20] KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	Ck 986 len	(R,K)[20] (K)[20]	KKKKKK	KKKK	Ċ.	× ~		*	σ		~	X.	KKK	837		<b>7</b>	X X	KKK	
aw38834  k	KKK	22		KKKKKKKKKKKKKK	{20} KKKKKKKKKKKKKKKKK	2799 len:	R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	4687 len:	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	6650 len: 2	(R,K)(20) (K)(20) KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20] KKKKKKKKKKKKKKKKKKKK	(K)[20] KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20}
peptide used in peptide m	! Aaw38833 Delivery peptide used in peptide XK	Askard Delivery portide god to	amboose perively bebuide used in	KXK	XX	Aaw38835 Delivery peptide used in peptide	KKXK	KXK	XK	Aaw38836 Delivery peptide used in peptide	KKKXK .	KKXX		XK	Aaw38837 Delivery peptide used in peptide	KKKKX	KKKXK	KKXK	KXK	

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AAW38800 ck: 6625 len: 26
                                                                                                                                                               AAW38799 ck: 4663 len: 25
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                                                                                                                                                                                                                                                                                          AAW38798 ck: 2776 len: 24 ! Aaw38798 Delivery peptide used in pepti
                                                                                                                                                                                                                                                                                                                                                                                                AAW38797 ck: 964 len: 23
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KKKK KKKKKKKKKKKKKKKKKK KXK
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(K){20}
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! Aaw38800 Delivery peptide used in peption
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AAW38803
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K KKKKKKKKKKKKKKKKKKKKKKKKKK
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K KKKKKKKKKKKKKKKKKKKK KKKWK
                                                      ck: 2961 len: 29 '! Aaw38803 Delivery peptide used in peptide
                        (R,K)[20]
(K)[20]
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(K){20}
KKKKKKKKKKKKKKKKKKKKKK KKKKK
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(K){20}
                                                                                                                                                                                                                                                                          len: 28
                                                                                                                                                                                                                                                                     ! Aaw38802 Delivery peptide used in peptide
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AAW38805 ck: 7560 len: 31
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(K){20}
      (K) (20)
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AAW38807 ck: 2459 len: 33
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                                                                  (K){20}
                                                                                ck: 9972 len: 32
                                                                                                                                                                                                                                                              (R,K){20}
(K){20}
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(K){20}
(K){20}
                                                                                                                ! Aaw38807 Delivery peptide used in peptide
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(K){20}
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KKKKK KKKKKKKKKKKKKKKKKKKKKKKK
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                      (K)(20)

KK KKKKKKKKKKKKKKKKKKKK KKVTK
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(K){20}
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AAW38882 ck: 979
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KKKK KKKKKKKKKKKKKKKKKKK VTK
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KKKK KKKKKKKKKKKKKKKKKKK KVTK
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                                                     (K){20}
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KKK KKKKKKKKKKKKKKKKKKK KKKKK
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KK KKKKKKKKKKKKKKKKKKK KKKVT
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KK KKKKKKKKKKKKKKKKKKKK KKKK
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K KKKKKKKKKKKKKKKKKKKKKKKKKKK
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(K){20}
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(K)[20]
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                                                                                                                                                                        len: 28
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(K){20}
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                                                                                      AAW38883 ck: 3174 len: 29
                                                                                                                  AAW38848 ck: 3193 len: 37
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                                                    (R,K){20}
(K){20}
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                                                                                    ! Aaw38883 Delivery peptide used in peptid
                                                                                                                                                                                                                                                                                                                                            ! Aaw38848 Delivery peptide used in peptid
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AAW38884 ck: 5444 len: 30
                                                                       17: KKKKK KKKKKKKKKKKKKKKKKK XK
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KKKKKKKKKKKKKKKKKKK KKKK
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14:
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             (K){20}
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KKKKK KKKKKKKKKKKKKKKKKK VTK
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KKKK KKKKKKKKKKKKKKKKKKKKKKKKKK
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KKK KKKKKKKKKKKKKKKKKKK KKKKV
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                                                                                                                                                                                                       (R,K){20}
(K){20}
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(K){20}
             12:
                         (K){20}
                                        10:
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                                                                                                                                                                           AAW38851 ck: 2007 len: 40
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AAW38852 ck: 5095 len: 41
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10: KKKKK KKKKKKKKKKKKKKKKKKK VTK
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               (K) [20]
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                              (K)[20]
KK KKKKKKKKKKKKKKKKKKK KKKKK
                                              (K){20}
                                                             len: 32
                                                                                                                                                                                                                                                            ! Aaw38886 Delivery peptide used in peptid
                                                                                 ! Aaw38852 Delivery peptide used in peptid
```

5.

(K) [20]

```
12:
                                                                                                                                                                                                                                                   (K){20}
                                                                                                                                                                                                                                                                 10:
                                                                                                                   AAW38887 ck: 2704 len: 33
                                                                                                                                (K){20}
                                                                                                                                             (K){20}
                                                                                                                                                                       17: KKKKK KKKKKKKKKKKKKKKKKK KKKXK
                                                                                                                                                                                   (K){20}
                                                                                                                                                                                                (K){20}
                                                                                                                                                                                                                          6.
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                                                                                     2:
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                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                           (K){20}
                                 (K){20}
                                                                                                                                                                                                                                       (K){20}
                                                                                                                                                                                                                                                                (K)(20)
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                                              (K)(20)
KKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                           (K){20}
                                                                       (K){20}
                                                                                   (K) {20}
                                                                                                                 ! Aaw38887 Delivery peptide used in peptide
```

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(K){20}
                                          17:
                                                      16:
                                                                15: KKKK KKKKKKKKKKKKKKKKK KKKKK
                                                                            (K){20}
                                                                                       (K){20}
                                                                                                                                                                                                                                                                         (K){20}
                                                                                                                                                                                                                                                  AAW38853 ck: 8258 len: 42
                                                                                                                                      4..
                                                                                                                                                                                                                                                                                     (K){20}
                                                                                                                                                 (K){20}
                                                                                                                                                                                   (K){20}
KKKK KKKKKKKKKKKKKKKKKKK KKKK
                                                                                                                                                                                              (R,K){20}
(K){20}
(K) {20}
                                                                                                                                                                                                                                                 ! Aaw38853 Delivery peptide used in peptid
```

21: KKKKK KKKKKKKKKKKKKKKKKK XK

```
(K){20}
                                                                                                                                                                         (K){20}
                                                                                                                                                                                                         AAW38854 ck: 1496 len: 43
                                                                                                                                                                                                                                                                                                                                                                                AAW38888 ck: 5274 len: 34
                                                                                                   ω
..
                                                                                                                   2
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(K){20}
                                (K){20}
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KKKKK KKKKKKKKKKKKKKKKKKK KKKKK
                (K)(20)
                                                (K)(20)
                                                                                                                                                                                                                                         (K)(20)
                                                                (K){20}
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KKK KKKKKKKKKKKKKKKKKK KKKK
                                                                                                                                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                                                                                                          (K)(20)
                                                                                                                  (R,K){20}
(K){20}
                                                                                                                                                                                                                                                                                                                                                          ! Aaw38854 Delivery peptide used in peptide
                                                                                                                                                                                                                                                                                                                                                                             ! Aaw38888 Delivery peptide used in peptide
```

```
(K){20}
                                                                                                                                                                                                          ω
••
                                                                                                        AAW38889 ck: 7919 len: 35
                                                                                                                                               (K){20}
                                                                                                                                                         18: KKKKK KKKKKKKKKKKKKKKKK KKKKX
                                                                                                                                                                   17: KKKKK KKKKKKKKKKKKKKKKKK KKKKK
                                        6:
                                                  ..
                                                                                2
                                        (K){20}
                                                            (K){20}
                                                                               (R,K){20}
(K){20}
                                                                                                      ! Aaw38889 Delivery peptide used in peptid
```

```
(K){20}
                                                                                                                                                     (K){20}
                                                                                                                                                                           (K){20}
                                                                                                                                                                                                                         AAW38890 ck: 639
                                                                                                                              AAW38891 ck: 3434 len: 37
                                                                                                                                                                                                   12: KKKKK KKKKKKKKKKKKKKKKK KKVTK
                                                                                                                                                                                                                                                10: KKKKK .KKKKKKKKKKKKKKKKKK KKKKV
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  (K){20}
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                        (K)[20]
KKK KKKKKKKKKKKKKKKKKKK KKKK
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K KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                       (R,K){20}
(K){20}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36
                                                                                                                            ! Aaw38891 Delivery peptide used in peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ! Aaw38890 Delivery peptide used in peptide
13: KKKKK KKKKKKKKKKKKKKKKKKK KKKVT
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                                                                                                                                                                                          5:
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```

(K){20} AAW38892 ck: 6304 len: 38 (K){20} (K) {20} 10: KKKKK KKKKKKKKKKKKKKKKKK KKKKK (K){20} (K)(20)
KKKKK KKKKKKKKKKKKKKKKKKKKKKTT

! Aaw38892 Delivery peptide used in pepti

 $(\kappa)$ {20} (K){20} (K){20} (R,K){20}
(K){20}

10: KKKKK KKKKKKKKKKKKKKKKKK KKKKK (K) [20]

```
AAW38894 ck: 2269 len: 40
                                              (K){20}
                                                                                  (K){20}
                                                                                                                     (K)(20)
                                                                                                                                                                                                                                                         (K){20}
                                                                                                                                                                                                                                              AAW38893 ck: 9249 len: 39
        ::
                                                                                                                                 ..
                                                                                                                                                                                                        ω
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                                                                                                                                                                                                       (R,K){20}
(K){20}
KKKKKKKKKKKKKKKKKKKK KKKK
(K)[20]
                     ! Aaw38894 Delivery peptide used in peptide
                                                                                                                                                                                                                                            ! Aaw38893 Delivery peptide used in peptide
```

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	••			ω	2:	1:	AW		7 :	 0	5:		ω 	2:	1:	10:	9:	8.	7 :	9	5 :	<u></u>	ω	2:
	KKKKK	KKKK	KKK	KK	*		AAW38895	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKK	KKK	χ. X	<b>×</b>
(K) (20)	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKK	ck: 5364 len: 41	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K) (20) KKKKKKKKKKKKKKKKKKK	(K){20}	(K) {20}	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	KKKKKKKKKKKKKKKKKK
	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	! Aaw38895 Delivery pept:	VTK	KVTK	KKVTK	KKKVT	KKKKV	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKK	XXXXX	KKKKK	KKKKK	KKKKK

ide used in peptid

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(K)(20)
                                                                                                                                                      (K){20}
                                                                                                                                                               AAW38896 ck: 8534 len: 42 | Aaw38896 Delivery peptide used in peptide
                                                                                                             (K){20}
                                                                                                                              5.
              1.
                                       4
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                                                                         2
                                                                                                                                                                                       (K){20}
                                                        (K){20}
                                                                (K)(20)

KK KKKKKKKKKKKKKKKKKKKK KKKK
                                                                         (K){20}
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13:	12:	11:	10:	9:	œ .:	7:	<b>б</b> :	<del>ن</del> ::	<del>4</del> ::	ω 	2:	1:	AAW	20:	19:	18:	17:	16:	15:	14:	13:	12:	11:
KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKK	XXX	KK	×		AAW38897	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	
(K){20} K KKKKKKKKKKKKKKKKKKKK KKKKK	(K){20} K KKKKKKKKKKKKKKKKKKK KKKKK	(K){20}	(K){20}	(K)(20) K KKKKKKKKKKKKKKKKKK KKKKK	(K)(20)	(K){20} K KKKKKKKKKKKKKKKKKKKK KKKKK	K KKKKKKKKKKKKKKKKKK KKKKK	K KKKKKKKKKKKKKKKKKK KKKKK	KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	K KKKKKKKKKKKKKKKKKK KKKKK (K) {20}	(K){20}	(R,K)(20) (K)(20) KKKKKKKKKKKKKKKKKKKKK KKKKK	ck: 1779 len: 43 ! Aaw38897 Delivery	(K){20}	(K){20}	(K)(20) K KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20) K KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	K KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	K KKKKKKKKKKKKKKKKKK KKKKK	K KKKKKKKKKKKKKKKKKKK KKKKK	K KKKKKKKKKKKKKKKKKKK KKKKK	(K){20}	KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
													peptide used										
													ed in peption										
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(K) (20)

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14:
                              (K){20}
                                           12:
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                                                                              9:
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                   (K){20}
                                          (K)[20]
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                                                                                         (K){20}
                                                                                                    (R,K){20}

(K){20}
(K) {20}
                                                                                                                                                                                         ! Aaw38898 Delivery peptide used in peptide
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(K){20}
14: KKKKK KKKKKKKKKKKKKKKKKK WK
                            (K){20}
                                         (K){20}
                                                       (K){20}
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                                                                                                                                                                                                                                                  20: KKKKK KKKKKKKKKKKKKKKKKKK KKVTK
                                                                     16: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK
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                                                                                                                             (K){20}
                                                                                                                                           (K){20}
                                                                                                                                                         (K){20}
                                                                                                                                                                       ! Aaw38809 Delivery peptide used in peptid
```

AAW38810 ck: 370 len: 36

! Aaw38810 Delivery peptide used in peptid

1:

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(K){20}
                                                                                                                                                                                            (K){20}
                                                                                                                                                                                                          AAW38811 ck: 3157 len: 37
                                                                                                                                                  (K){20}
15: KKKKK KKKKKKKKKKKKKKKK WK
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                            (K)(20)
                                                        (K){20}
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                                                                                    K KKKKKKKKKKKKKKKKKKK KKKKK
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                                                                                                                          (R, K) {20}
                                                                                                                                 ! Aaw38811 Delivery peptide used in peptide
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(K){20}
                                                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                     (K){20}
                                                                                                                                                                                                                                                            16: KKKKK KKKKKKKKKKKKKKKKK WK
                                                                                                                                                                                                               12: KKKKK KKKKKKKKKKKKKKKKKK KKKKW
                                                                                                                                                                                        AAW38812 ck: 6019 len: 38
                                                                              2
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                                                                                         (K){20}
KKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                        (K)(20)
                                                                                                                                                              ! Aaw38812 Delivery peptide used in peptic
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(K){20}
                                                     AAW38814 ck: 1968 len: 40
                                                                    (K){20}
                                                                                                                                  (K){20}
                                                                                                                                                   (K){20}
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                                                                                                                                                                                 (K){20}
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17: KKKKK KKKKKKKKKKKKKKKKKK WK
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KKKKK KKKKKKKKKKKKKKKKKK KKKKK
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(K){20}
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                               (R,K){20}
(K){20}
                                                                                                                                                                                                                                                                                                                                          ! Aaw38814 Delivery peptide used in peptide
                                                                                                                                                                                                                                                                                                                                                             1 Aaw38813 Delivery peptide used in peptide
```

7:	6.	<b>5</b>	<b>4</b>	ω 	2:	<b>:</b>	AAW	19:	18:	17:	16:	15:	14:	13:	12:	11:	10:	9:	æ :-	7:	6:	ن. 	4.
KKKKK	KKKKK	KKKK	KKK	KK	*		AAW38815	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKK	KKK
(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKK	ck: 5055 len: 41	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K)[20] KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK
KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKK	! Aaw38815 Delivery	WK	KWK	KKWK	KKKWK	KKKKW	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK

peptide used in peptid

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AAW38816 ck: 8217 len: 42
                   (K)(20)
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                              (K){20}
                                                  (K){20}
                                                                       (K){20}
KK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                (K){20}
                                                                                          (R,K){20}
(K){20}
KKKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                        ! Aaw38816 Delivery peptide used in peptide
```

														•										
12:	11:	:	10:	9	œ 	7:	6:	5:	<u></u>	ω 	2:	1:	AAW	21:	20:	19:	18:	17:	16:	15:	14:	13:	12:	11:
KKKKK	KKKKK		KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKK	KKK	Ķ.	*		AAW38817	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
KKKKKKKKKKKKKKKK KKKKK	KKKKKKKKKKKKKKKKK KKKKK  (K){20}		(K){20} KKKKKKKKKKKKKKKKK KKKKK	(K)(20) KXKKKKKKKKKKKKKKK KKKKK	(K)[20] KKKKKKKKKKKKKKKKK KKKKK	KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20] KKKKKKKKKKKKKKKKKK KKKKK	KKKKKKKKKKKKKKKKK KKKKK	(K)(20) KKKKKKKKKKKKKKKKK KKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKK KKKKK	(R,K)(20) (K)(20) KKKKKKKKKKKKKKKKK KKKKK	ck: 1454 len: 43   Aaw38817 Delivery peptide used in peptid	(K){20} KKKKKKKKKKKKKKKKKK WK	(K){20} KKKKKKKKKKKKKKKKK KWK	(K)(20) KKKKKKKKKKKKKKKKKK KKWK	KKKKKKKKKKKKKKKKKK KKKWK	KKKKKKKKKKKKKKKK KKKKW	(K)[20]	KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20]	(K){20}	(K)(20)	(K)(20)

YKAKK K  KAKKK K  KKKKK K  KKKKK K  KKKKK K	21: YEDES AAW24450 4: YKA 5: YKAK	21: KKKKK 22: KKKKK	KKKKK	.7: KKKKK	15: KKKKK	13: KKKKK
(K) [20] KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)[20] (K)[20] (K)[20] (K)[20] (K)[20] (K)[20] (K)[20] (K)[20] (K)[20] (K)[20]	(K){20} (K){20} (K){20} (K){20} K KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} K KKKKKKKKKKKKKKKKKK KKWK (K){20} K KKKKKKKKKKKKKKKKKK KKWK	(K)(20) K KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) (20) (K) (20) (K) (20)	(K){20}  (K){20}  (K){20}
KKKKK KKKKK KKKKKK KKKKKK KKKKKK KKKKKK	(NA) binding p	KWK WK  ! Aaw24865 Bifunctional peptide I for binding	KKKWK	KKKKK	KKKKK	KKKKK

	11: K	10: K	9: 🛪	8: <b>x</b>	7: K	6: <b>X</b>	5:	4 ::	<b>.</b>	2:	1:	AAW21	24: K	23 : X	22: K	21: K	20: <b>x</b>	19: K	18: K	17: K	16: K	15: K	14: K
1	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKK	KKK	K K	×		21590	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
	(K){20} KKKKKKKKKKKKKKKKKKK	(K)[20] KKKKKKKKKKKKKKKKKKK K	(K)[20] KKKKKKKKKKKKKKKKKK KK	(K)(20) KKKKKKKKKKKKKKKKKK KKK	(K)[20] KKKKKKKKKKKKKKKKKK KKKK	(K)(20) KKKKKKKKKKKKKKKKKK KKKKK	(K)(20) KKKKKKKKKKKKKKKKK KKKKK	(K){20} KKKKKKKKKKKKKKKKKK KKKK	(K)(20) KKKKKKKKKKKKKKKKKK KKKKK	(K){20} KKKKKKKKKKKKKKKKK KKKKK	(R,K)(20) (K)(20) KKKKKKKKKKKKKKKKKK KKKKK	ck: 4875 len: 30 ! Aaw21590 Antibiotic potentiating peptide	(K){20} KKKKKKKKKKKKKKKKK WK	(K)[20] KKKKKKKKKKKKKKKKK KWK	(K){20} KKKKKKKKKKKKKKKKK KKWK	(K)[20] KKKKKKKKKKKKKKKKK KKKWK	(K)(20) KKKKKKKKKKKKKKKKK KKKKW	(K)[20]	(K)(20)	(K)(20)	(K){20} KKKKKKKKKKKKKKKKKK KKKKK	(K)(20) KKKKKKKKKKKKKKKKKK KKKKK	KKKKKKKKKKKKKKKKK KKKKK

AAW21591 ck: 5075 len: 434 ! Aaw21591 Antibiotic potentiating peptide

(R,K)(20)

	24:	23.	22:	21:	20:	19:	18:	17:	16:	15:	14:	13:	12:	11:	10:	9:	8:	7:	<b>б</b>	5:	<u></u>	ω	2:	1:
	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKK	KKK	K K	*	
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268: K	267: K	266: K	265: K	264: K	263: K	262: K	261: K	260: K	259: K	258: K	257: K	256: K	255: K	254: K	253: K	252: F	251: F	250: 1	249: H	248: F	247: F	246: H	245: 1	244: 1
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(K) [20]	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) {20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK
	KKKKK	KKKKK .	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK								

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KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) {20} KKKKKKKKKKKKKKKKKKKKK	(K) (20)	(K)(20) KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) {20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K)(20) KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	KKKKKKKKKKKKKKKKKK
KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK

	389:	388:	387:	386:	385:	384:	383:	382:	381:	380:	379:	378:	377:	376:	375:	374:	373:	372:	371:	370:	369:	368:	367:	366:
	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
(K){20}	(K) [20] KKKKKKKKKKKKKKKKKKK !	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20}
	KKKKK	KKKKK	KKKKK	XXXXX	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK

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(K){20}
                                                  (K){20}
                                                                                                                                                                                                                                                                                    392: KKKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                           408: KKKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                    399: KKKKK KKKKKKKKKKKKKKKKKKK KKKKK
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AAW48808 ck: 9658 len: 56
                                                                                                          16: KKKKK KKKKKKKKKKKKKKKKKKK KKYCG
                                                                                                                                             (K){20}
                                                                                                                                                                                                  AAW65939 ck: 1569 len: 40
                                                                                                                                                               14: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                     (K){20}
TKKK KKKKKKKKKKKKKKKKKKK KKKKK
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TKK KKKKKKKKKKKKKKKKKKK KKKKK
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                                                                                                                                                                                                                                                                                                                                                                                 (K) [20]
                                                                                                                                                                                                                                                                                                                                                                                             (R,K){20}
                                                                                                                                                                                                                                                                                                                                                                                                       ! Aaw65939 Polylysine peptide NBC32. 11/1:
                                                                      ! Aaw48808 Homo sapiens clone CG109_1 pro
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(K){20}
                                                                                                                                                                                                                                                                                                  40:
                                                                                                                                                                AAB59105 ck: 8456 len: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY12950 ck: 5821 len: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (R,K){20}
(K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                       AAY07213 ck: 2211 len: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY43246 ck: 9752 len: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW45802 ck: 7664 len: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW45800 ck: 9056 len: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW45801 ck: 9500 len: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37: REKKK KKKKKKKKKKKKKKKKKKKK
                                                   (R,K){20}
(K){20}
YEDES KKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                ck: 4945 len: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (R,K)[20]
             ! Aab53249 Human colon cancer antigen protein
                                                                                                                                                          ! Aab59105 Breast and ovarian cancer associat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ! Aaw45801 One chain of a bombesin dimer. 6/
                                                                                                                                                                                                                                                                                                                                       ! Aay12950 Amino acid sequence of a human se
                                                                                                                                                                                                                                                                                                                                                                                                                  ! Aay07213 Peptide transfection vector #I. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ! Aay43246 Cell-surface molecule binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! Aaw45802 One chain of an alpha-MSH recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! Aaw45800 One chain of an alpha-melanocyte
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(K){20}
                                                                                                       (K){20}
                                                                                                                                                          AAB53800 ck: 296 len: 69
                                                                                                                                                                                                                                                                                                                                                 AAB53659 ck: 3850、len: 184  ! Aab53659 Human colon cancer antigen prot
                                                                                                                                                                                                                                                                                                                                32: KKKKK KKKKKKKKKKKKKKKKK NXGGG
                                                                                                                                                                                                                                                                                                                                                                   30:
                                                                                                                                                                                                                                                                                                                                                                                                                     (K){20}
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                                                                                                                                                                                                  (K){20}
KKKKK KKKKKKKKKKKKKKKKKK XGGRF
                                                                                                                                                                                                                                                                                                                                                                  (K){20}
KKKK KKKKKKKKKKKKKKKKKKKK KXGGR
                                                                                                                                                                                                                                    (K){20}
K KKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                              (R,K) (20)
(K) (20)
                                                                                                                                                                                                                                                                                      (K) (20)
                                                                                                                                                                                ! Aab53800 Human colon cancer antigen prot
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(K){20}
                                                        26: CLLKK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                          (K){20}
                                                                                                                            (K){20}
                                                                                                                                                                                                                                                                                                                                                                                      (R,K)[20]
(K)[20]
(K)[20]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB53977 ck: 7756 len: 75
                                                                                                                                                                                                             30: KKKKK KKKKKKKKKKKKKKKKKKK XKXKK
                                                                                                                                                                                                                                                                               28: DSKKK KKKKKKKKKKKKKKKKKK KKXKX
                                                                                                                                                                                                                                                                                                                  27: CDSKK KKKKKKKKKKKKKKKKKKK KKKXK
                                                                                                                                                                                                                                                                                                                                                    26: DCDSK KKKKKKKKKKKKKKKKKKK KKKKX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40: KKKKK KKKKKKKKKKKKKKKKKKK XGGPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36: KKKKK KKKKKKKKKKKKKKKKKK KKKKX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33: KKKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30: KKKKK KKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB53806 ck: 8373 len: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39: KKKKK KKKKKKKKKKKKKKKKKK KXGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38: KKKKK KKKKKKKKKKKKKKKKKK KKXGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34: KKKKK KKKKKKKKKKKKKKKKKK KKKKK
(K) {20}
                                                                                                                                                                       l Aab53977 Human colon cancer antigen protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 ! Aab53806 Human colon cancer antigen proteir
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AAB53980 ck: 881
                          49: KKKKK KKKKKKKKKKKKKKKKKK GGPVX
                                                  (K){20}
48: KKKKK KKKKKKKKKKKKKKKKKKK KGGPV
                                                                            (K){20}
47: KKKKK KKKKKKKKKKKKKKKKK KKGGP
                                                                                                     (K){20}
                                                                                                                                                                                 (K) [20]
                                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                   (K){20}
                                                                                                                                                                                                                                                             40: KKKKK KKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                      38: KKKKK KKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                       36: KKKKK KKKKKKKKKKKKKKKKKK KKKKK
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                                                                                                                                                                                                                                                                                                                                                                                                                 (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                           33: KKKKK KKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29: KKKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         len: 45
! Aab53980 Human colon cancer antigen pro
```

(R,K){20}
(K){20}
(K){40}

(K) (20)

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93:
                                                                                                                                                      (K){20}
                                                                                                                                                                                                                                                                                                                                                         AAB56121 ck: 5941 len: 125 ! Aab56121 Human secreted protein sequence
                                                                                                                                                                                                                                         30:
                                                                                                                                                                                                                                                           (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                         11: FOKKK KKKKKKKKKKKKKKKKKK KXGGR
                                                                                                                                                                                                   32: KKKKK KKKKKKKKKKKKKKKKKKK GGRF
                                                                                                                                                                                                                                                                                                                                      (K){20}
                                                                                                                                                                                                                                                                                                                                                                                   AAB54314 ck: 6235 len: 55
                                                                                                                                                                                                                                                                                                                                                                                                      (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                            10: SFQKK KKKKKKKKKKKKKKKKKKK KKXGG
                                                                                                                (K){20}
                                                                                                                                                                                                                                                                             (K){20}
XKKKK KKKKKKKKKKKKKKKKKKK KKKKG
                                     (K){20}
                                                         (K){20}
                                                                                                                                                                                                                                        (K){20}
                                                                                                                                                                                                                                                                                                                    ! Aab54314 Human pancreatic cancer antigen pı
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(K){20}
            (K)(20)
                                    (K){20}
                                                            100: KKKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                    (K){20}
                                                                                                                                                                                                                           101: KKKKK KKKKKKKKKKKKKKKKKK KKGGP
                                                                                                                                                                                                                                       100: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKGG
                                                                                                                                                                                                               (K){20}
                                                                                    AAB27956 ck: 6732 len: 139 ! Aab27956 Human secreted protein SEQ ID N
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(K){20}
                                                                                                                                                                                                                                                                                                       114: KKKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                          (K){20}
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                                                                                                                                                                                                          (K){20}
119: KKKKK KKKKKKKKKKKKKKKKKK K
                                                                                                                                                                                                                                               (K){20}
                                                                                                                                                                                                                                                                  116: KKKKK KKKKKKKKKKKKKKKKKKK KKKK
                                                                                                                                                                                                                                                                                     (K){20}
                                                                                                                                                                                                                                                                                                                                             (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                           (K){20}
         AAB41457 ck: 4536 len: 168
                           (K){20}
                                                                 (K){20}
                                                                                                                                           (K){20}
                                                                                                                         (K){20}
                                                                                                                                                                     AAB39140 ck: 9531 len: 66
                                                                                                                                                                   ! Aab39140 Human secreted protein #48. 2/200:
      ! Aab41457 Human ORFX ORF1221 polypeptide sec
            ω
..
(K) [20]
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(R,K){20}
(K){20}
196: NILFW KKKKKKKKKKKKKKKKKKKK XXGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB44188 ck: 4991 len: 43
                                                                                                                                 AAB43835 ck: 4025 len: 223 ! Aab43835 Human cancer associated protei
                                                                                                                                                                                                  AAB43641 ck: 5216 len: 133 ! Aab43641 Human cancer associated protei
                                                                                                                                                                                                                               (K){20}
42: RCLKK KKKKKKKKKKKKKKKKKKK K
                                                                                                                                                                                                                                                                                     AAB42889 ck: 6432 len: 62
                                                                                                                                                                                                                                                                                                                                                                                     (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                (K){20}
82: DVLQK KKKKKKKKKKKKKKKKKKKK K
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB42786 ck: 4959 len: 102 ! Aab42786 Human ORFX ORF2550 polypeptide
! Aab44188 Human cancer associated protei
                                                                                                                                                                                                                                                                                                                                                      ! Aab42889 Human ORFX ORF2653 polypeptide
```

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46:
                   AAB23591
                                           (K){20}
16: GSGSK KKKKKKKKKKKKKKKKKKKKK G
                                                                                                                                                             15:
                                                                                                                                                                                                                                                                             45:
                                                                                                                                                                                                                                                                                                      44:
                                                                                                                                                                                                                                                                                                                                43:
                                                                                                        AAB23586 ck: 58
                                                                                                                                                                                                                                                                                                                                                         42:
                                                                                                                                                                                                                                                                                                                                                                                 (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                             40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB23585 ck: 9893 len: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB34331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB44380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (K)(20)
GSGSK KKKKKKKKKKKKKKKKKKKK G
                                                                                                                                                           (K){20}
KKKKK KKKKKKKKKKKKKKKKK K
                                                                                                                                                                                                                                                                                                                                                       (K)[20]
                                                                                                                                                                                                                                                                           (K){20}
KPKKK KKKKKKKKKKKKKKKKKKK KKKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKKK KKKKKKKKKKKKKKKKKK KKGRP
                 ck: 7684 len: 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 8490 len: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                             ck: 8131 len: 66
(R,K)[20]
                                                                                                        len: 36
            ! Aab23591 Modified fibre protein encoded in
                                                                                                   ! Aab23586 GsK21 linker peptide. 1/2001
                                                                                                                                                                                            ! Aab23585 AsK21 linker peptide. 1/2001
                                                                                                                                                                                                                                                                                                                                                                                                                                          l Aab34331 Human secreted protein sequence er
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ! Aab44380 Human secreted protein encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>,,,</u>
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(K) (20)

597: GSGSK KKKKKKKKKKKKKKKKKKKKK GSAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    597: GSGSK KKKKKKKKKKKKKKKKKKKKK GSYSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            597: GSGSK KKKKKKKKKKKKKKKKKKKK GSYSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (R,K){20}
(K){20}
83: RKRQQ KKKKKKKKKKKKKKKKKKKK
                                                                                                 84: KRQQK KKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                         AAY98493
                                                                                                                                                                                                   AAG00834
                                                                                                                                                                                                                                                                                                                                         (R,K){20}
(K){20}
26: AAAAA KKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB23594 ck: 2612 len: 640 ! Aab23594 Modified fibre protein encoded
                                                                                                                                                                                                                                                                                                                                                                                                AAB13783 ck: 4553 len: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB13780 ck: 7317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB23593 ck: 2249
                                                                                                                                                                                                                                                                                                  AAB13784 ck: 4126 len: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB23592 ck: 7647 len: 630
(R,K){20}
(K){20}
YKA KKKKKKKKKKKKKKKKKKKK KKKKK
                                                        ck: 8137 len: 45
                                                                                                                                                                                                 ck: 6330 len: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                         len: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             len: 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ! Aab23592 Modified fibre protein encoded
                                                                                                                                                                                                ! Aag00834 Human secreted protein, SEQ ID
                                                       ! Aay98493 Peptide #5 used in nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ! Aab23593 Modified fibre protein encoded
                                                                                                                                                                                                                                                                                               ! Aab13784 Soluble tandem HA/ pK peptide c
                                                                                                                                                                                                                                                                                                                                                                                            ! Aab13783 Soluble tandem pEA/ pK peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Aab13780 Soluble peptide antigen pK. 11/
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(K){20}
           (K)(20)
19: PYKAK KKKKKKKKKKKKKKKKKKKKK KKKKK
                        AAY99495 ck: 4361 len: 59
                                                     (K)(20)
24: KKKKK KKKKKKKKKKKKKKKKK WK
                                                                  (K){20}
                                                                                          (K){20}
                                                                                                      (K){20}
                                                                                                                               (K){20}
                                                                                                                                            (K)(20)
                                                                                                                                                                                             (K){20}
                                                                                                                                                                                                          15: KKKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                               ! Aay98495 Nuclear ligand used in nucleic ac
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	228:	227:	226:	225:	224:	223:	222:	221:	220:	219:	ABG	118:	117:	116:	115:	114:	113:	112:	111:	110:	109:	108:	107:	106:
	KKKKK	KKKKK	KKKKK	RKKKK	RRKKK	ERRKK	EERRK	EEERR	EEEER	вевев	ABG05367	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	EKKKK	EEKKK	EEEKK	EEEEK	EEEEE
	(R,K){20}	(R,K)(20) KKRRRRRRRRRRRRRKK KKKKK	(R,K){20}	(R,K){20}	(R,K){20} KKKKKRRRRRRRRRRRRR RKKKK	(R,K){20}	(R,K){20}	(R,K)(20)	(R,K){20}	(R,K)(20) (R,K)(20) RRKKKKKKKKRRRRRRRRR RRRRR	ck: 6907 len: 808 ! Abg05367 Novel human diagnostic protein #53	(R,K)(20)	(R,K)(20) KKKKKKKKKKKKKKKKKK KEEEE	(R,K){20}	(R.K)(20)	KKKKKKKKKKKKKKKKKK KKKE	(R,K)[20]	(K)[20] KKKKKKKKKKKKKKKK RKKKK	KKKKKKKKKKKKKKKKK KRKKK	(K)[20] KKKKKKKKKKKKKKKKK KKRKK	KKKKKKKKKKKKKKKK KKKRK	(K){20} KKKKKKKKKKKKKKKK KKKKR	(K)[20] KKKKKKKKKKKKKKKK KKKK	(K)[20] KKKKKKKKKKKKKKKKK KKKKK
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54	53	52	51	50	49		AB	208	207	206	205	АВ	260	259	258	237	236	235	234	233	232	231	230	229

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(R,K){20}
229: KKKKK RRRRRRRRRRRRRRKKKK KKKKK
(R,K){20}
(R,K){20}
9: KKKKT RKKRKKRKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                 (R,K){20}
)8: SSRRR RRRRKKKRKKKKKKKRRRRR QQQQQ
                                                                                                                                                                                                                                                                                                                                                                        (R,K){20}
(R,K){20}
S: KKKSS RRRRRRKKKKKKKKKKRR RRRQQ
                                                                                                        .BG06513 ck: 2934 len: 154 ! Abg06513 Novel human diagnostic protein
                                                                                                                                                                                                                                                                                                    (R,K){20}
7: KSSRR RRRRKKKRKKKKKKKKKRRRR RQQQQ
                                                                                                                                                                                                                                                                                                                                      (R,K){20}
6: KKSSR RRRRRKKKRKKKKKKKKRRR RRQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58: KKKKN KKKKKKKKKKKKKKKKKKK KKNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (R,K){20}
RRRRR RRRRRRRKKKKKKKKKKKK NKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (R,K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (R,K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                    .BG06375 ck: 7807 len: 2,570 ! Abg06375 Novel human diagnostic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (R,K){20}
3: KRRRR RRRRRRRRRRKKKKKKKKKKKKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (R,K)[20]
82: KKRRR RRRRRRRRRRRRKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (R,K){20}
(RKKRR RRRRRRRRRRRRRKKKKKK KKKKK
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65:	64:	63 :	62:	61:	60:	59:	58:	57:	56:	55:	54 :	ABG	65:	64:	63:	62:	61:	60:	59:	58:	57:	56:	55:
KKKKK	KKKKK	KKKKK	XXXXX	RKKKK	RRKKK	RRRKK	ERRRK	EERRR	EEERR	DEEER	DDEEE	ABG07742	KKKKK	RKKKK	KRKKK	KKRKK	KKKRK	RKKKR	KRKKK	KKRKK	RKKRK	KRKKR	KKRKK
(R,K){20} KKKKKRKKKKKKKKKKKKK	(R,K){20} KKKKKKRKKKKKKKKKKKKKK	(R,K){20} KKKKKKKKKKKKKKKKKKK	(R,K){20} KKKKKKKKKKKKKKKKKKKK	(R,K)(20) KKKKKKKKKKKKKKKKKKKKK	(R, K) {20} KKKKKKKKKKKKKKKKKKKKK	(R, K) {20} KKKKKKKKKKKRKKKKKKRK	(R, K) {20} KKKKKKKKKKKKKKKKKK	(R, K) {20}	(R,K){20}	(R,K){20} RRKKKKKKKKKKKKKKKKKKK	(R,K){20} (R,K){20} RRRKKKKKKKKKKKKKKKKKKK	ck: 8672 len: 502	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(X){20}	(K){20}	(K){20}	(K){20}	RKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)[20]	(R,K){20}	(R,K){20}	(R,K){20}
KKNIL	KKKNI	XXXXX	KKKKK	KKKKK	KKKKK	XXXXX	XXXXX	RKKKK	KRKKK	KKRKK	KKKRK	Abg07742 Novel human diagnostic protein #77	SEXDR	KSEXD	KKSEX	KKKSE	KKKKS	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
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ABG11241 ck: 3870 len: 121 ! Abg11241 Novel human diagnostic protein
                                                                                                                                                                         (R,K){20}
76: KRKKK RKKKKKKKKKKKKKKKKKKKKKKKKEE
                                                                                                          (K){20}
                                                                                                                                           78: KKKRK KKKKKKKKKKKKKKKKKKK KEEEE
                                                                                                                                                                                                                                          (R,K){20}
                                                                                                                                                                                                                                                                                                          72: EKEKK RKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                          ABG10053 ck: 3274 len: 189 ! Abg10053 Novel human diagnostic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG10052 ck: 7107 len: 39 ! Abg10052 Novel human diagnostic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67: KKKKK KKKRKKKKKKKKKKKKKKK NILYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7: KKKKK KKKKKKKKKKKKKKKKKK EKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (K){20}
QKKK KKKKKKKKKKKKKKKKKKK KKEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (K){20}
QKK KKKKKKKKKKKKKKKKKKKK KKKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (K)(20)
QK KKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (K){20}
Q KKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (R,K){20}
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60: KKKKK KKKKKKKKKKKKKKKKKKK KKKKK
                  (K){20}
57: KKKKK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                 (K){20}
                                                                                                               56: XKKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                               49: KKKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                             (K){20}
                                                                                                                                                                                                           (K){20}
                                                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                                         49: KKKKK KKKKKKKKKKKKKKKKKK XEKEK
                                                                                                                                                                                                                                                                                                                                                         (K)(20)
                                                                                                                                                                                                                                                                                                           ABG11242 ck: 4493 len: 100 ! Abg11242 Novel human diagnostic protein #1:
                                                                                                                                                                                                                                                                                                                                          (K) (20)
                                                                                                                                                                                                                                                                                                                                                                         46: KEEKK KKKKKKKKKKKKKKKKKK KKKXE
(K){20}
                                              (K){20}
                                42:
                                                             38:
                                                                                                             36: EEKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                            (K){20}
```

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(R){20}
                  ABG11245 ck: 2517 len: 85
                                                                                                      69: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                         68: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                              (K){20}
                                                                                                                                                                                                                           71: KKKKK KKKKKKKKKKKKKKKKKKK NPIFF
                                                                                    (K)(20)
                                                                        (K) [20]
                                            1 Abg11245 Novel human diagnostic protein
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80:	79:	40:	39:	38:	37:	36:	ABG1	59:	58:	57 :	56:	55:	54:	53:	ABC:	52:	51:	50:	49:	48:	47:	46:	45:
EEEEK	EEEEE	EKKKK	REKKK	KREKK	EKREK	KEKRE	ABG11266	***	KKKK	EKKKK	KEKKK	EKEKK	KEKEK	EKEKE	ABG11250	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
(R,K){20} KKKKKRKRKRKKKKKKKKK	(R,K){20} KKKKKKKRKRKRKKKKKKKKKK	(K){20}	(K){20}	(K){20}	(K){20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKK	ck: 9563 len: 146	(R,K)[20] KKKKKKKKKKKKKKKKKKKKKK	(R,K){20} KKKKKKKKKKKKKKKKKKKKK	(R,K){20} KKKKKKKKKKKKKKKKKKR	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(R, K) {20} (K) {20}	ck: 4343 len: 92	(K) [20] KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK
KRKKK	RKRKK	EFFEE	KEEEE	KKEEE	KKKEE	KKKKE	Abgl1266 Novel human diagnostic protein #11	EMALQ	KEMAL	KKEMA	RKKEM	KRKKE	KKRKK	KKKRK	! Abg11250 Novel human diagnostic protein #11	GRKTD	KGRKT	KKGRK	KKKGR	KKKKG	KKKKK	XXXXX	KKKKK

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(R,K){20}
                                        (R,K){20}
                                                      (R,K){20}
                                                                    (R,K){20}
                                                                                 (R.K){20}
                                                                                                ABG11277 ck: 8026 len: 1,080 ! Abg11277 Novel human diagnostic protein
                                                                                                                                                           (R,K){20}
93: RKRKK KKRKRKRKRKKKKKKKKKKK EKKKK
                                                                                                                                                                        86: KKKKK RKRKRKKKKKRKRKRKKKKK KKKKK
                                                                                                                                                                                                                                                                                       (R, K) (20)
                                                                                                                                                                                                                                                                                                                                 81: EEEKK KKKKKRKRKRKKKKKKKKKK RKKKK
                                                                                                                                                                                                                                                                         (R,K){20}
```

	114	11	112:	111:	110:	109:	ъ	ь	بنو	_	<b></b>			>	727:	726:	725:	724:	723:	722:	72	720:	719:
	••	.13: VK					ABG11734	13: RR	12: GR	11: RG	10: RR	9: RR	8: KR	ABG11732							21: KK		
	KKK .	VKKKK	SVKKK	LSVKK	MLSVK	OMLSV		RRRRR	GRRRR	RGRRR	RRGRR	RRRGR	KRRRG		KKKRK	KKKKR	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKK
(K) [20]	(R,K)	(R,K)	(R,K)	(R,K)	(R,K)	(R, K)	ck: 4	(R)(	(R){	(R){	(R)	(R){	(R,K) (R) RRRRF	ck:	(R,K)	(R,K)	(R,K)	(R,K)	(R,K)	(R,K)	(R,K)	(R,K)	(R,K)
20)	(20) KKKKI	(20) KKKK	{20} KKKK	{20} KKKK	{20} (KKKK)	(20) (20) (RKKK	4548	20} RRRR	20} {RRRR	20)	20}	20}	{20} 20} \RRRR	2886	{20} (XKKK	(20)	(20)	(20)	(20) (RKKK	(20) (KRKK	{ 20 }	{20}	(20) (KRKK
	KKKK	KKKK	KKKK	KKKK	KKKK	KKKKK	len:	RRRRR	RRRRR	RRRRF	RRRRF	RRRRF	RRRRF	len:	KKKKK	KKKKK	KKKK	KKKK	KKKK	KKKK	KKKK	KKKKK	RKKKK
	(R,K){20} KKKKK 'RKKKKKKKKKKKKKKKKKKK	(R, K) {20}	(R,K){20}	(R,K){20} KKKRKKKKKKKKKKKKKKKK	(R,K){20} KKKKRKKKKKKKKKKKKKKK	(R,K) [20] (R,K) [20] KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	142	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R,K){20} (R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	56	(R,K){20} KRKKKKKKKKKKKKKKKKKK	(R,K){20}	(R,K){20}	(R,K){20}	(R,K){20} KKRKKRKKKKKKKKKKKKKK	(R,K){20} KKKRKKRKKKKKKKKKKKKK	(R,K){20} KKKKRKKKKKKKKKKKKKK	(R,K){20}	(R,K){20}
	(K KK													-									K KK
	KKKKL	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	Abg11734	PKQKN	RPKQK	RRPKQ	RRRPK	RRRRP	RRRRR	Abg11732	EERRK	KEERR	KKEER	KKKEE	KKKKE .	KKKKK	KKKKK	KKKKK	KKKKK
														1732									
							Novel							Novel human									
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(R,K)[20]
(R,K)[20]
27: GRERE RRRRKRKRRRKRRRKRRRR RRRRG
                                  ABG22638 ck: 4197 len: 896 ! Abg22638 Novel human diagnostic proteir
                                                                36: KKKKK KKKKKKKKKKKKKKKKKKK QLSLV
                                                                                           (K){20}
                                                                                                                                                                               (K)[20]
32: KKFKK KKKKKKKKKKKKKKKKKKKK KKKKQ
                                                                                                                                                                                                                                        33: KKKKK KKKKKKKKKKKKKKKKKK KERRT
                                                                                                                                                                                                                                                                                                                                                                                             (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                         (K){20}
ERRKK KKKKKKKKKKKKKKKKKKK KKRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (K){20}
                                                                                                                                                                                                            ABG22512 ck: 8641 len: 856 ! Abg22512 Novel human diagnostic proteir
                                                                                                                                                                                                                                                                                                         (R,K)(20)
34: KKKKK KKKKKKKKKKKKKKKKKKK ERRTA
                                                                                                                                                                                                                                                                                                                                                                 (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG11738 ck: 3009 len: 567 ! Abg11738 Novel human diagnostic proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (K)[20]

(K)[20]
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(R,K)(20)
104: KKKKK KKKKKKKKKKKKKKKK E
                                                                         103: KKKKK KKKKKKKKKKKKKKKKKK KE
                                                                                                   (R,K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (R,K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (R,K)[20]
231: ERRRR RKRKRRKRRKRRKRRRRRR GXEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (R,K){20}
228: RERER RRRRKRKRRRKRRRKRRRRR RRRGX
             ABG26489 ck: 9923 len: 120 ! Abg26489 Novel human diagnostic protein #26
                                                                                                                                                                                    .66
                                                                                                                                                                                                                 98:
                                                                                                                                                                                                                                            97:
                                                                                                                                                                                                                                                                                                                             94:
                                                                                                                                                                                                                                                                                                                                                                                                          95:
                                                                                                                                                                                                                                                                                                                                                        93:
                                                                                                                                                                                                                                                                                                                                                                                   92:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG26488 ck: 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG26213
                                                                                                                                                                                                               (R,K)[20]
RRRKK KKKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                   (R,K)[20]
                                                                                                                                                                                                                                                                    (R,K)(20)
                                                                                                                                                                                                                                                                                                                          (R,K)(20)
RERRR RRKRKRRKRRKRRKRRRRRR RGXEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (R,K){20}
ERERR RRRKRKRRRKRRKRRRRR RRGXE
                                                                                                                                                                                                                                                                                                                                                        EEERR
(R,K)[20]
                                                                                                                                                                                                                                                                                                                                                      (R,K){20}
RRRKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ck: 6773 len: 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                len: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                             ! Abg26488 Novel human diagnostic protein #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! Abg26213 Novel human diagnostic protein #20
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ABG26491 ck: 8179
                                                                                                                                 (R)[20]
76: RGRRR RRRRRRRRRRRRRRRRR R
                                                                                                                                               (R){20}
                                                                                                                                                                                                                                                                               (R,K)[20]
74: GRRRR RRRRRRRRRRRRRRKK KEEEE
                                                                                                                                                                                                                                                                                              73:
                                                                                                                                                                                                                                                    ABG26490 ck: 4146 len: 96
                                                                                                                                                                                                                                                                  (R,K){20}
                                                                                                                                                                                                                                                                                                           72:
                                                                                                                                                                                                                                                                                                                         71:
                                                                                                                                                                                                                                                                                                                                       (R,K)[20]
RGRRR RRRRRRRRRRRRRRRRRK KKEEE
                                                                                                                                                                                                                                                                                                           len: 109
                                                                                                    ! Abg26491 Novel human diagnostic protein
                                                                                                                                                                                                                                                   ! Abg26490 Novel human diagnostic protein
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	40:	39:	38:	37:	36:	35:	3 <b>4</b> :	ω ω 	32:	31:	30:	29:	28:	27 :	ABG	33:	32:	31:	30:	29:	ABG	83:	82:
	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	KRRRR	EKRRR	KEKRR	EKEKR	KEKEK	EKEKE	ABG26493	ERRRR	EERRR	KEERR	KKEER	KKKEE	ABG26492	KRKKK	KKRKK
	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R,K){20} (R,K){20} KRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 4204 len: 80	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRR	(R,K){20} (R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 5234 len: 68	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK
_	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	Abg26493 Novel human diagnostic protein #26	GKKDG	RGKKD	RRGKK	RRRGK	RRRRG	Abg26492 Novel human diagnostic protein #26	GNLSV	KGNLS

																	•						
70:	69:	68:	67 :	66:	65:	64:	63:	62:	61:	ABG2	53:	52:	51:	50:	49:	48:	47:	46:	45:	44:	43:	42:	41:
RRRRR	RRRRR	RRRRR	RRRRR	KRRRR	EKRRR	EEKRR	KEEKR	KKEEK	EKKEE	26496	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR
(R)(20)	(R){20}	(R)[20]	(R)(20)	(R)[20] REFERERERERERERERERERERERERERERERERERER	(R)[20] RREKRREKREKREKERER REKER	(R)(20)	(R)(20) REBERERERERERERERERERERERERERERERERERER	(R)[20] (RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K)(20) (R,K)(20) KRRERRERERERERERERERERERERERERERERERERE	ck: 8829 len: 90 ! Abg26496 Novel human diagnostic protein	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RERERERERERERERERE RENTN	(R)[20]	(R)[20]	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20)	(R)[20] RERERERERERERERERERERERERERERERERERERE	(R){20}	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] R RRRRRRRRRRRRRRRRRR RRRRR	(R)(20)	R RRRRRRRRRRRRRRRRRRRR RRRRR

6:	44: RRRRR	43: RRRRR	42: RRRRR	41: RRRRR	40: RRRRR	39: RRRRR	38: RRRRR	37: RRRRR	36: RRRRR	35: RRRRR	34: RRRRR	33: RRRRR	32: RRRRR	31: RRRRR	30: RRRRR	29: RRRRR	28: DRRRR	27: EDRRR	26: EEDRR	25: GEEDR	24: EGEED	ABG26497
	(R) (20) (R) (20) (R) (20) RRHRHRHRHRHRHRHRRR		(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRERERERERERERERERERERERERERERERERERER	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] R RRRRRRRRRRRRRRRRRRRRR	(R){20} R RRRRRRRRRRRRRRRRRRRR	(R)[20] R RERERERERERERERERERE	(R)[20] R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	· (R){20} R RRRRRRRRRRRRRRRRRRR	(R){20} R RRRRRRRRRRRRRRRRRRRR	(R){20} R RRRRRRRRRRRRRRRRRRRRR	(R){20} R RRRRRRRRRRRRRRRRRRRR	(R){20} R REFERERERERERERERERE	(R){20} R RRRRRRRRRRRRRRRRRRRR	(R,K){20} (R){20}  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 9186 len: 115
RRRRR	RRRRR	RRRRR	RRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	! Abg26497 Novel human diagnostic protein #26

71:	70:	69:	68:	67 :	66:	65:	64:	63:	62:	61:	60:	59:	58:	57:	56:	55:	54:	53:	52:	51:	50:	49:	48:	47:
RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR
(R){20} RRRRRRRRRRRRRRRRRRR I	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR

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(R){20}
                                                                                                                (R){20}
                                                                                                                          (R)[20]
83: RRRRR RRRRRRRRRRRRRRRRRRRRRTT
                                                                                                                                    (R){20}
                                                                                  ABG26498 ck: 7156 len: 140 ! Abg26498 Novel human diagnostic protein #26
                                                                                                                                                                 (R){20}
(R){20}
48: RRRRR RRRRRRRRRRRRRRRRR GRRRR
                                                                                                            37:
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(R,K){20}
113: RRRRR RRRRRRRRRRRRRRRRRRRRK YKYLE
                                                                                                                                             (R){20}
         (R){20}
                  (R){20}
                           (R){20}
                                     (R){20}
                                                                                   (R)[20]
                                                                                                     ABG26500 ck: 7252 len: 78
                                                                                            ! Abg26500 Novel human diagnostic proteir.
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(R) [20]  RRESER RRERRERRERRERRERRERRERRERRERRERRERRER		ABG26501 72: KEEKE 73: EEKEK 74: EKEKK 75: KEKKK 76: EKKKK	CK: 1730 len: 182 (R,K)[20] KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	! Abg26501 Novel human diagnostic  KKKKE  KKKEE  KKEEE  KEEEE  KEEEE
6: RSERR RÖRRÜRRERRERRERRERRERRERRERRERRERRERRERRER	ω ω 	GRRRS RRRSR	RRRKRRKKRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	RRRRR
(R) (20) 8: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	35 36	RRSRR	(R) (20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	RRRRR
9: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	37 38	SRRRR	(R) (20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	RRRRR
(R) (20)  (RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	39	RRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	RRRRR
(R) [20]  2: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRR	140:	RRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	RRRRR
2: RRRRR (R) (20) 3: RRRRR (R) (20) 4: RRRRR (R) (20) 4: RRRRR (R) (20) 5: RRRRR (R) (20) 6: RRRRR (R) (20) 6: RRRRR (R) (20) 6: RRRRR (R) (20) 7: RRRRR (R) (20) 8: RRRRR (R) (20) 8: RRRRR (R) (20) 9: RRRRR (R) (20)	141:	RRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	RRRRR
3: RRRRR (R) (20) (R) (20) (R) (20) 4: RRRRR (R) (20) 5: RRRRR (R) (20) 6: RRRRR (R) (20) 6: RRRRR (R) (20) 7: RRRRR (R) (20) 8: RRRRR (R) (20) 8: RRRRR (R) (20) 9: RRRRR (R) (20)	142:	RRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	RRRRR
4: RRRRR (R)(20) 5: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	143:	RRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	RRRRR
5: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	144:	RRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	RRRRR
(R) [20]	5	RRRRR	(R)(20) RRRRRRRRRRRRRRRRRRRR	RRRRK
(R)(20) 7: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	6	RRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	RRRKY
(R){20} 8: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	147:	RRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	RRKYP
(R){20} 9: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	48:	RRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	RKYPM
(R,K){20} 0: RERER RERERERERERERERERERERERE	9	RRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	KYPMW
	0	RRRRR	(R,K){20} RRRRRRRRRRRRRRRRRK	AMMAA

69:	68:	67:	66:	65:	64:	63:	62:	61:	60:	ABG	69:	68:	67:	66:	65:	64:	63:	62:	61:	60:	59:	ABG
RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	GRRRR	EGRRR	EEGRR	EEEGR	KEEEG	ABG26505	RKKKK	RRKKK	RRRKK	RRRRK	RRRRR	RRRRR	GRRRR	EGRRR	EEGRR	EEEGR	EEEEG	ABG26502
(R,K){20} RRRRRRRRRRRRRRRRKKK EEEEE	(R,K)[20] RRRRRRRRRRRRRRRRKK KEEEE	(R,K){20} RRRRRRRRRRRRRRRRRK KKEEE	(R){20} RRRRRRRRRRRRRRRRRRR KKKEE	(R)(20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRERRERRERRERRERRER REKKK	(R)[20] RRRRRRRRRRRRRRRRRR RRKK	(R)[20] RRRRRRRRRRRRRRRRRRR RRRK	(R)(20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K)[20] (R)[20] RRHRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 4704 len: 93 ! Abg26505 Novel human diagnostic protein	(R,K){20} KKKKKKKKKKKKKKKKK EYFQT	(R,K)[20] KKKKKKKKKKKKKKKKKK KEYFQ	(R,K){20}	(R,K)(20)	(R,K){20}	RKKKKKKKKKKKKKKKKK KKKKK	RRKKKKKKKKKKKKKKKK RKKKK	RRRKKKKKKKKKKKKKKK KRKKK	(R,K)(20)	RRRBBKKKKKKKKKKKKK KKKRK	(R,K)[20] (R,K)[20] RRRRRKKKKKKKKKKKKK KKKKR	ck: 3399 len: 101   Abg26502 Novel human diagnostic protein

64	63:	62:	61:	60:	ABG2	62:	61:	60:	59:	58:	57:	56:	55:	54:	53:	52:	51:	50:	49:	48:	47:	ABG 2
ERRRR	EERRR	EEERR	EEEER	EEEEE	6507	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	RKKKK	KRKKK	RKRKK	KRKRK	RKRKR	KRKRK	EKRKR	KEKRK	EKEKR	KEKEK	EKEKE	ABG26506
(R,K){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR		(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} (R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 9838 len: 109	(R, K) { 20 }	(R,K){20}	(R,K){20}	(R,K)[20]	(R,K){20}	(K){20}	(K){20}	(K){20}	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKKK	(R,K){20} RKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20}	(R,K)[20]	(R,K)[20]	(R,K)[20]	(R,K){20} (R,K){20}	ck: 3684 len: 85
KERKK	KKERK	RKKER	RRKKE	RRRKK	! Abg26507 Novel human diagnostic protein #2	YTWIN	KNWTV	TWNXX	KKKNM	KKKKN	RKKKK	KRKKK	KKRKK	KKKRK	KKKKR	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	! Abg26506 Novel human diagnostic protein #26

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(R,K)(20)
(R,K)(20)
199: EEEEE KKKKKKRKKKKKKKKKKKKK EEEKK
                                       ABG26513 ck: 3117 len: 265 ! Abg26513 Novel human diagnostic protein
                                                              69: KKKKK KKKRKKKKKKKKKKKKKKK NILYR
                                                                                                                                                                                                                      (R,K){20}
                                                                                                                                                                                                                                                                                                                                                 60: ERRRK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                               ABG26508 ck: 4488 len: 121 ! Abg26508 Novel human diagnostic protein
                                                                                                                                                                             ABG26510 ck: 3426 len: 74
                                                                                                                                                                                                                                                                                    (R,K)[20]
KKKKK KKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                            (K){20}
                                                                                                                                                                            ! Abg26510 Novel human diagnostic protein
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264: RKKKK	263: SRKKK	262: ESRKK	261: EESRK	260: KEESR	259: KKEES	ABG26515	193: RRRRR	192: RRRRR	191: RRRRR	190: RRRRR	189: RRRRR	188: RRRRR	187: RRRRR	186: GRRRR	185: RGRRR	184: RRGRR	183: ERRGR	182: EERRG	ABG26514	225: EEKKK	224: EEEKK	223: KEEEK	222: KKEEE
(R,K){20}	(R,K){20}	(K){20}	(K)[20]	(K){20}	(R,K){20} (R,K){20} RKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 7288 len: 389	(R,K){20} RRERRERRERRERRERREKK	(R,K){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) RRARRARRARRARRARRARRARRARRARRARRARRARRA	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] R RERERERERERERERERERERERERERERERERERER	(R, K) [20] (R) [20] RRHRHRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 9106 len: 218	(R,K)(20)	(R,K)(20)	(K){20}	E KKKKKKKKKKKKKKKKKKK KRKEE
RNKNK	KRNKN	RKRNK	KRKRN	KKRKR	KKKRK	! Abg26515 Novel human diagnostic protein #26	ERISS	KERIS	KKERI	RKKER	RRKKE	RRRKK	RRRK	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	! Abg26514 Novel human diagnostic protein #26	EEEEE	KEEEE	RKEEE	KRKEE
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735:	734:	733:	732:	731:	730:	729:	728:	727:	726:	725:	ABG	54:	53:	52:	51:	50:	49:	48:	47:	46:	45:	ABG	265:
RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	ERRRR	EERRR	EEERR	EEEER	еееее	26518	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	ERRRR	EERRR	EEERR	EEEER	EEEEE	26516	KKKKK
(R){20} R RRRRRRRRRRRRRRRRRR KKKRK	(R)(20) R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} R RRRRRRRRRRRRRRRRRRRRRRRRRRRKKK	(R)(20) R RRRRRRRRRRRRRRRRRR RRRKK	(R)(20) R RRRRRRRRRRRRRRRRRR RRRRK	(R)(20) R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) R ERRERERERERERERERE FERRE	(R)(20) R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K)[20] (R)[20] E RÄRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 8431 len: 761 ! Abg26518 Novel human	(R,K)(20) R RRRRRRKKRKRKRKKKK TKTKT	(R,K){20} R RRRRRRRKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)[20] R HRRRRRRRKKRKRKRKRKK KKTKT	(R,K){20} RRRRRRRRRKKRKRKRKRKR KKKTK	(R,K){20} RRRRRRRRRRRKKRKRKRK RKKKT	(R,K){20}	(R,K)[20] RRRRRRRRRRRRRKKKKKK KKKK	(R,K)(20) RRRRRRRRRRRRRRKKRKR KRKRK	(R,K){20}	(R,K)(20) (R,K)(20) E RRRRRRRRRRRRRRRRRKKR KRKRK	ck: 2295 len: 91 ! Abg26516 Novel human	(R,K){20} K KKKKKKKKKKKKKKKKKKKKRKR NKNKK
											diagnostic p											diagnostic	
											rotein											protein	

50:	49:	48:	47:	46:	45:	44:	<b>4</b> 3:	42:	41:	40:	39:	38:	37:	36:	3 5 	ABG	741:	740:	739:	738:	737:	736:
RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	ERRRR	EERRR	EEERR	EEEER	88888	ABG26520	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR
(R) (20) RREKRERERERERERE (R) (20) REFERERERERERERERERERERERERERERERERERER	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRHRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRR	(R,K)(20) (R)(20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 2487 len: 99	(R,K){20} RRRRRRRRRRRRKKKRKK	(R,K){20} RRRRRRRRRRRRRRKKKRK	(R,K)[20] RRRRRRRRRRRRRRRKKKR	(R,K)[20] RRRRRRRRRRRRRRRRKKK	(R,K)[20] RRRRRRRRRRRRRRRRRKK	(R,K){20} RRRRRRRRRRRRRRRRRRK KKRKK
RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	Abg26520 Novel human diagnostic protein #26	z	KN	KKN	RKKN	KRKKN	KKRKK

75:	74:	73:	72:	71:	70:	69:	68:	67:	66:	65:	64:	63:	62:	61:	60:	59:	58:	57:	56:	55:	54:	53:	52:
RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR
(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R) [20] RRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
RRRKI	RRRRK	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR

96: K	50: E	49: E	48: E	47: E	46: H	ABG26522	328: H	327: H	326: 1	325: F	324: F	323: }	322: F	321: (	320: 1	319: 1	318: 1	317: 1	ABG26521	79: 1	78: 1	77: 1	76: 1
KKEEG	ERRRR	EERRR	EEERR	EEEER	BEEEE	522	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	GKKKK	EGKKK	EEGKK	EEEGK	EEEEG	5521	RRRRR	RRRRR	RRRRR	RRRRR
(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR		(R,K){20} RRRRRRRRRRRRRRRRRRK	(R){20} RRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R,K){20} (R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 2060 len: 152	(R,K)(20) KKKKKKKKKKKKKRRRKKKK	(R,K){20} KKKKKKKKKKKKKKKRRRKKK	(R,K){20} KKKKKKKKKKKKKKKKRRKK	(R,K){20} KKKKKKKKKKKKKKKKKRRRK	(R, K){20} KKKKKKKKKKKKKKKKKKRRR	(R, K) {20} KKKKKKKKKKKKKKKKKKRR	(R, K) {20} KKKKKKKKKKKKKKKKKKKR	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 482 len: 367	(R,K)(20) RRRRRRRRRRRRRRRRRK	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R)[20] RERERERERERERERERERERE REKI
RRRRR	EGEEG	KEGEE	KKEGE	RKKEG	RRKKE	! Abg26522 Novel human diagnostic protein #26	EQQLE	KEOOL	KKEQQ	KKKEQ	KKKKE	RKKKK	RRKKK	RRRKK	KRRRK	KKRRR	KKKRR	KKKKR	! Abg26521 Novel human diagnostic protein #26	Н	X.	RKI	RRKI
			μ		1																		

	50:	49:	<b>4</b> 8:	ABG	ω 	ABG26	113:	112:	111:	110:	109:	108:	107:	106:	105;	104:	103:	102:	101:	100:	99:	98:	97:
	EEERR	EEEER	EEEEE	ABG26526	RD	26525	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	GRRRR	EGRRR	EEGRR	KEEGR
(R,K){20}	(R,K){20} RRRRRRRRRRRRRRRRRKK	(R,K){20} RRRRRRRRRRRRRRRRRRK	(R,K){20} (R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 1887 len: 115	(R,K)(20) (R,K)(20) RRRKKKKKKKKKKKKKKKKKKK	ck: 5433 len: 103	(R,K){20} RRRRRRRRRRRRRRRRRRK	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRR
	REKKK	KREKK	KKREK	! Abg26526 Novel human diagnostic protein	EEBEE	! Abg26525 Novel human diagnostic protein	ERERE	KERER	RKERE	RRKER	RRRKE	RRRRK	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRR	RRRRR	RRRRR	RRRRR	RRRRR

176: RRRRR RERERERERERERERERERERERERERERERE	175: REBER ERERERERERERERERERERERERERERERERE	(R) [20]	(R){20}	(R)(20) 173: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRM	(R)[20] 172: RERER ERERERERERERERERERERERERERERERER	(R){20} 171: GRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 170: RGRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 169: RRGRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) 168: RRRGR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 167: GRRRG RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	96: KKRKK KKKKKKKKKKKKKKK EEEEE	(K) (20) 95: KKKRK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	94: RKKKR KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	93: KRKKK RKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	92: KKRKK KRKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	91: EKKRK KKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	90: KEKKR KKKRKKKKKKKKKKKKKKKKKKKKKKKKKKKK	89: EKEKK RKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	88: KEKEK KRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	87: EKEKE KKRKKRKKKKKKKKKKKKKKKKKKKKKKKKKK	ABG26528 ck: 2237 len: 215 ! Abg26528 Novel human diagnostic protein #26	82: EEEEE KKKKKKKKKKKKRRRRRR GRRRM	ABG26527 ck: 5586 len: 122 ! Abg26527 Novel human diagnostic protein #26	51: EERRR RRRRRRRRRRRRRRRRKKR EKKKS
(R){20} 54: REKRR REKRERREKRERREKER REKEE	(R){20} 53: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 52: ERRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	51: DERRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	50: KDERR RŘRŘRŘRŘRŘRŘRŘRŘRŘRŘRŘRŘ	49: EKDER RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	EEKDE		ABG26531 ck: 7434 len: 126 ! Abg26531 Novel human diagnostic protei	(R,K){20} 379: RRRRR RRRRRRRRRRRRRRRRR NTSLR	(R)(20) 378: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) 377: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 376: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 375: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) 374: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 373: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 372: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 371: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 370: ERRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) 369: EERRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 368: EEERR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) 367: EEEER RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	1 (R,K)[20] (R)[20] 366: EEEEE RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ABG26530 ck: 5729 len: 404 ! Abg26530 Novel human diagnostic protei	(R){20} 177: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRR

52:	51:	ABG2	167:	166:	165:	164:	163:	162:	161:	160:	159:	158:	157:	156:	155:	154:	153:	152:	ABG	57:	56:	55:
RRRTR	RRRRT	26533	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	KRRRR	KKRRR	KKKRR	EKKKR	EEKKK	EEEKK	EEEEK	EEEEE	26532	RRRRR	RRRRR	RRRRR
(R)[20] RRERRERRERRERRERRERRERRERRERRERRERRERRE	(R,K){20} (R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 5900 len: 101	(R){20} RRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRR	(R) (20) RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} KRRRRRRRRRRRRRRRRRRRRRR	(R,K)[20] KKRRRRRRRRRRRRRRRRRRRR	(R,K){20} (R,K){20} KKKRRRRRRRRRRRRRRRRRRR	ck: 9650 len: 225	(R){20} RRRRRRRRRRRRRRRRRRRR	(R)(20) RRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
RRRRK	RRRRR	Abg26533 Novel human diagnostic protein #26	NKQTK	RNKOT	RRNKQ	RRRNK	RRRRN	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	! Abg26532 Novel human diagnostic protein #26	EBEBB	REEEE	RREEE

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58:
                                                                                                                                                                                                                  (R,K){20}
57: RRRRR RRRRRRRRRRRRRRRRK KKPTS
                                                                                                                        (R,K)[20]
59: RRRRR RRRRRRRRRRRRRRRKKK PTSRV
                                                                                                                                                                                                                                        (R){20}
                                                                                                                                                                                                                                                  ABG26534 ck: 1919 len: 113
                                                                                                                                                                                                                                                              (R,K)(20)
RRRRR RRRRRRRRRRRRRRRKK KPTSR
                                                                                                                                                                                                                             ! Abg26534 Novel human diagnostic protein
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(R) {20}	(R)(20) 428: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) 427: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) 426: RRERE REFERERERERERERERERERERERERERERER	(R)[20] 425: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 424: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 423: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 422: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R) (20) 421: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 420: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) 419: ERRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) 418: EERRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	417: EEERR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 416: EEEER RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} (R){20} 415: EEEEE RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ABG26535 ck: 2214 len: 472 ! Abg26535 Novel human diagnostic protein #26	55: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	54: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	53: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	52: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	51: KKKKR KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	50: KKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	49: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	48: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	47: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
60: KEKET KRRRRRKKKKKKKKKKKKKKKKKKKKKKKKKKK		ABG26538 ck: 5732 len: 98   Abg26538 Novel human diagnostic proteir	(K) (20) 486: RKKKK KKKKKKKKKKKKKKKKK TRKKK	(K) (20) 485: KRKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 484: KKRKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 483: EKKRK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20) 482: EEKKR KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R.K){20} 481: EEEKK RKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)(20) 480: KEEEK KRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	479: KKEEE KKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R)(20) 407: EQERR RRRRRRRRRRRRRRRRRRR EEEEE	(R)(20) 406: AEQER RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K)[20] (R)[20] 405: GAEQE RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ABG26537 ck: 2429 len: 573 ! Abg26537 Novel human diagnostic proteir	(R)[20] 438: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 437: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) 436: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 435: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 434: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 433: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 432: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 431: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 430: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	429: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR

(R)(20)  (R)(20)  (R)(20)  EEERR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(F)	(K){20} 77: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} RKKKK KKKKKKKKKKKKKKKKKK	(K)(20) KRKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} KKRKK KKKKKKKKK	(K){20 KKKRK KKKKKKK	(K){2	(R,K){	(R,K)	RRKKK KKRKI	RRRKK KKKR	RRRRK KKK	(R, I	(R, KRRRR RKK	TKRRR RRK	(R, ETKRR RRR	(R, KETKR RRR	EKETK RRR
	(R,K){20} (R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K)[20 KKKKKKK	(K)(2)	(R,K){	(R,K)		(R,K	(R, K	(R,	(R,	(R,	(R,	(R,	(R,
		~	KKK	KKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K)[20] KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(R,K){20} RKKKKKKKKKKKKKKKKKKKK	(R,K){20} KRKKKKKKKKKKKKKKKKKK	(R,K){20} KKRKKKKKKKKKKKKKKKKK	(R,K)[20] KKKRKKKKKKKKKKKKKKKK	(R,K)[20] KKKKRKKKKKKKKKKKKKKK	(R,K){20} KKKKKRKKKKKKKKKKKKK	(R,K){20} RKKKKKRKKKKKKKKKKKKK	(R,K){20} RRKKKKKRKKKKKKKKKKKK	(R,K){20}	(R,K){20} RRRRKKKKKKKKKKKKKKKKK	(R,K){20} RRRRRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
,	RRRR	GY ! Abg26539 Novel human diagnostic protein #26	KGY	KKGY .	KKKGY	KKKKG	XXXXX	KKKKK	KKKKK	KKKKK .	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	XXXXX

35: 36: 37: 38: 39: 39: 39: 40: 41: 42: 43: 43: 44: 43: 44: 44: 45: 46: 46: 46: 46: 46: 46: 46: 46: 46: 46	34	
14 BB 19 BB 17 6 BB 17 16 BB 17 17 17 17 17 17 17 17 17 17 17 17 17		
RRRRRR RRRRRR RRRRRR RRRRRR RRRRRR RRRRR	RRRRR	
RRIEBERRRRERRERRERRERRERRERRERRERRERRERRERR		

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281: KKKKK KKKKKKKKKKKKKKKKKK KGKKG
                                                                                                                        (K){20}
                                                                                                                                               276: RRKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                          (R,K)(20)

CR.K)(20)
92: EKKKK KKKKKKKKKKKKKKKKKKK KKKKK
            (K)[20]
(K)[40]
                                                            ABG26545 ck: 135 len: 119 ! Abg26545 Novel human diagnostic protein #20
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17:	16:	15:	14:	13:	12:	11:	10:	9:	σο 	7:	6:	5:	<b>4</b>	ω	2:	1:	ABG2	98:	97:	96:	95:	94:	93:
KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	RKKKK	RRKKK	RRRKK	KRRRK	KRRR	KRR	KR	*		26551	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK
(R,K){20} KKKKKKKKKKKKKKKKKKKKK	(R,K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} KKKKKKKKKKKKKKKKKKKKK	(R,K){20} KKKKKKKKKKKKKKKKKKKKK	(R,K){20} KKKKKKKKKKKKKKKKKKKKK	(R,K){20} KKKKKKKKKKKKKKKKKKK	(R,K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20}	(R,K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} KKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R, K) {20} RKKKKKKKKKKKKKKKKKKK	(R, K) (20) RRKKKKKKKKKKKKKKKKKKK	(R, K) {20} RRRKKKKKKKKKKKKKKKKKK	(R,K){20} (R,K){20} KRRRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 8976 len: 94	(K) (20) KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK
KKKKE	KKKKK	RKKKK	KRKKK	KKRKK	KKKRK	RKKKR	KRKKK	KKRKK	KKKRK	RKKKR	KRKKK	KKRKK	KKKRK	KKKKR	KKKKK	KKKKK	! Abg26551 Novel human d:	NT	KNF	KKNF	KKKNF	KKKKN	KKKKK

iagnostic proteir

ABG2	54:	53:	52:	51:	50:	49:	48:	47:	46:	45:	44:	43:	42:	41:	40:	39:	38:	37 :	ABG	21:	20:	19:	18:
26718	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	RKKKK	KRKKK	KKRKK	KKKRK	KKKKR	KKKKK	VKKKK	SVKKK	LSVKK	MLSVK	QMLSV	26717	KKKKK	KKKKK	KKKKK	KKKKK
ck: 9531 len: 141	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(R,K){20}	(R,K){20}	(R,K)(20)	(R,K){20}	(R,K){20}	(R,K){20} (R,K){20}	ck: 4415 len: 78	(R,K){20}	(R,K){20}	(R,K){20}	(R,K){20}
! Abg26718 Novel human diagnostic protein #26	LYFQT	KLYFQ	KKLYF	KKKLY	KKKKL	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK ·	KKKKK	KKKKK	KKKKK	XXXXX	! Abg26717 Novel human diagnostic protein #26	EKKKK	KEKKK	KKEKK	KKKEK

	53:	52:	51:	50:	49:	48:	47:	46:	4 5	44:	<b>4</b> 3:	42:	ABG	89:	88:	87 :	86:	85:	84:	83:	82:	81:	80:
	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	EKKKK	SEKKK	PSEKK	TPSEK	ETPSE	26719	KKKKK	KKKKK	KKKKK	KKKKK	RKKKK	PRKKK	RPRKK	ARPRK	VARPR	EVARP
(K) (20)	( KKKKKKKKKKKKKKKKKK KNPIF	(K)(20)	(K)[20] KKKKKKKKKKKKKKKKKKKKKKKKKKKKKNP	(K)[20] KKKKKKKKKKKKKKKKKKK KKKKN	(K){20}	K KKKKKKKKKKKKKKKKKK KKKKK	K KKKKKKKKKKKKKKKKKK KKKKK	(K)(20)	(K){20} K KKKKKKKKKKKKKKKKKK KKKKK	(K){20}	(K)(20)	(R,K)[20] (K)[20] E KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 72 len: 83   Abg26719 Novel human diagnostic protein	K KKKKKKKKKKKKKKKK EEEEE	(K)(20)	(K){20}	(K)(20)	(K)(20) K KKKKKKKKKKKKKKKKK KKKKE	(K){20}	(K)[20] K KKKKKKKKKKKKKKKKK KKKKK	(K)(20)	R KKKKKKKKKKKKKKKKK KKKKK	(R.K)(20) (R.K)(20)

54: KKKKK KKKKKKKKKKKKKKKKKKK NPIFF

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(K){20}
              (K){20}
                                                                                                                     32: KEKEK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                     33: KKKKK KKKKKKKKKKKKKKKKKKK FHFLL
                                                                                                                                                                                                    30: KKKKK KKKKKKKKKKKKKKKKKK KKKTH
                                                                                                                                                                                                                                                (K){20}
                                                                                                                                                                                                                                                                             (K){20}
                                                                                                                                                                                                                                                                                            ABG26721 ck: 287 len: 95
                                                                                                                                                                                                                                                                                                                                             ABG26720 ck: 3781 len: 57
                                                                                                                                                                                                                                                                                                                                           ! Abg26720 Novel human diagnostic protein #2
                                                                                                                                                                     ! Abg26721 Novel human diagnostic protein #20
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90:	: 68	88:	87:	49:	48:	47:	46:	45:	44:	ABG	54:	53:	52:	51:	50:	49:	48:	47:	46:	45:	44	43:	42:
EEKKK	EEEKK	KEEEK	EKEEE	KKKKK	EKKKK	EEKKK	KEEKK	KKEEK	KKKEE	26722	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK							
(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKK	ck: 4831 len: 127	(K)[20] KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) {20}	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K) (20) KKKKKKKKKKKKKKKKKKKK						
KKKKK	KKKKK	KKKKK	KKKKK	XEKEK	KXEKE	KKXEK	KKKXE	KKKKX	KKKKK	! Abg26722 Novel human diagnostic proteir	NKKKK	KNKKK	KKNKK	KKKNK	KKKKN	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK

```
ABG26723 ck: 7054 len: 98
                                                                                                  (K){20}
97: KKKKK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                     (K){20}
                                                                                                                                         ! Abg26723 Novel human diagnostic protein #20
```

70:	69:	68:	67:	66:	65:	64:	63:	62:	61:	60:	59:	58:	57 :	56:	55:	54:	53:	52:	51:	50:	49:	48:	47:
XXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K) [20] KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K)[20] KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K)[20] KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKKK	(K) {20} KKKKKKKKKKKKKKKKKKKKK	(K) {20}
OI I SX	KQLLS	KKQLL	KKKQL	кккко	KKKK	KKKKK	KKKKK	KKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX

ABG26724 ck: 9897 len: 295 ! Abg26724 Novel human diagnostic protein #26

```
(K){20}
                                                                                                                                                            (K){20}
                                                                                         269: KKKKK KKKKKKKKKKKKKKKKKK KKKK
                                                                                                                                                                                                                                               (K){20}
                                                                                                                                                                                                                                                                                                 264: KKKKK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                  (K){20}
                                                                                                                                                                                                                                                                                                                                   262: EEKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                   (K){20}
                                                                                                                                                                                                                                                                                                                                                                                    (K){20}
(K){20}
73: KEKKR KKKKKKKKKKKKKKKKKKKK KKKKK
                                                  72: KKEKK RKKKKKKKKKKKKKKKKKK KKKKK
                                  ABG26725 ck: 909
                                                                       len: 131 | Abg26725 Novel human diagnostic protein #26
```

252: KRKKK	251: RKRKK	250: KRKRK	249: RKRKR	248: KRKRK	247: RKRKR	246: KRKRK	245: RKRKR	244: ERKRK	243: KERKR	242: EKERK	241: KEKER	240: EKEKE	ABG26726	83: KKKKK	82: KKKKK	81: KKKKK	80: <b>кккк</b>	79: KKKKK	, 78: KKKK	77: RKKKK	76: KRKKK	75: KKRKK	74: EKKRK
(K) {20} KKKKKKKKKKKKKKKKKKKK	(K)[20] KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R, K) {20} RKKKKKKKKKKKKKKKKKKKK	(R,K){20} KRKKKKKKKKKKKKKKKKKK	(R,K){20} RKRKKKKKKKKKKKKKKKKKK	(R, K) {20} KRKRKKKKKKKKKKKKKKKKK	(R,K){20} RKRKRKKKKKKKKKKKKKKKKK	(R,K){20} KRKRKRKKKKKKKKKKKKKK	(R,K){20} RKRKRKKKKKKKKKKKKKK	(R,K){20} KRKRKRKRKKKKKKKKKKKK	(R,K){20} (R,K){20} RKRKRKRKRKKKKKKKKKKKK	ck: 9300 len: 677	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKK
KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK .	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	! Abg26726 Novel human	MLLLS	KMLLL	KKMLL	KKKML	KKKKM	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK

diagnostic protein

22	22	222:	22	22	21	218	21	216:	215:	>	265:	264:	263:	262:	261:	260:	25	258:	25	256	255	254:	25
4: ****	3: KKKKK	2: KKKKK	1: KKKKK	20: KKKKK	9: EKKKK	8: KEKKK	7: EKEKK	6: KEKEK	5: EKEKE	ABG26727	5: KKKKK	4: KKKKK	3: KKKKK	2: KKKKK	1: KKKKK	0: KKKKK	9: KKKKK	8: KKKKK	257: KKKKK	6: KKKKK	5: KKKKK	4: KKKKK	253: RKK#
(K)[20] KK KKKKKKKKKKKKKKKKK KKKKK	(K){20}	(K) (20)	(K) (20)	(K) (20)	(K) (20)	(K) (20)	(K){20}	(K){20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 813 len: 329 ! Abg26727 Novel human diagnostic	(R,K){20}	(R,K)[20] KK KKKKKKKKKKKKKKKKKK KLSLH	(R,K)[20]	AKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AKK KKKKKKKKKKKKKKKKKK KKKKL	(K){20}	(K){20}	(K){20}	(K)(20)	(K){20}	(K)(20)	(K){20}	RKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
··-	<u> </u>			- <del></del>				·		protein #26	<del>-</del>												
	1								1							H							

114 :	AAG6	41:	40:	39:	38:	37:	36:	35:	ABG	564:	563:	562:	561:	560:	559:	ABG	230:	229:	228:	227 :	226:	225:
TOLRO	5985	RRRRR	RRRRR	GRRRR	EGRRR	EEGRR	EEEGR	EEEEG	ABG28885	KKRKK	EKKRK	QEKKR	EQEKK	REQEK	EREQE	BG26879	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
(R, K) {20} (K) {20} KKKKKKKKKKKKKKKKKKKKK	ck: 8085 len: 154	(R,K){20} RRRRRRRRRRRRRRRRRKK	(R,K){20} RRRRRRRRRRRRRRRRRK	(R){20} RRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R,K){20} (R){20} RRERERERERERERERERERERERERERERERERERER	ck: 8668 len: 137	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} RKKKKKKKKKKKKKKKKKKK	(R,K){20} KRKKKKKKKKKKKKKKKKKK	(R,K)(20) (R,K)(20) KKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 2669 len: 800	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) (20) KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK
KKKKK	! Aag65985 B726P splice variant sequence.	K VLSPS	K KVLSP	R KKVLS	R RKKYL	R RRKKV	R RRRKK	R RRRRK	Abg28885 Novel human diagnostic protein	K QQEKE	K KQQEK	K KKQQE	K KKKQQ	K KKKKQ	K KKKK	! Abg26879 Novel human diagnostic protein	K TSQDA	K KTSQD	K KKTSQ	X XXXTS	K KKKKT	K KXKXK

(K) (20)

	23:	22:	21:	20:	19:	18:	17:	16:	15:	ABI	128	127	126	125	124	123	122	121	120	119	118	117	116	115
	RRKKK	RRRKK	RRRRK	RRRRR	GRRRR	: RGRRR	: RRGRR	: RRRGR	: RRRRG	АВВ27893	: KKKKK	: XKKKK	: KKKKK	: KKKKK	: KKKKK	: QKKKK	: RQKKK	: LRQKK	: QLRQK					
(R,K){20}	(R,K){20} KKKRKKKKKKKKKKRRRRR	(R,K){20} KKKKRKKKKKKKKKKKKRRRRR	(R,K){20} KKKKKRKKKKKKKKKKKRRRR	(R,K){20} KKKKKKKKKKKKKKKKKRRR	(R,K){20} RKKKKKKRKKKKKKKKKRR	(R,K)[20]	(R,K){20}	(R,K){20} RRRRKKKKKKKKKKKKKKKKKK	(R,K){20} (R,K){20} RRRRRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 5383 len: 86	(K){20}	(K)(20)	(K){20}	(K){20}	C KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK									
	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	KRRRR	KKRRR	! Abb27893 Human peptide #544 encoded by brea	XKKKK	KXKKK	KKXKK	KKKXK	KKKKX	KKKKK								

	57:	ABB2	45:	44:	43:	42:	41:	40:	39:	38:	37:	36:	35:	3 <b>4</b> :	33:	32:	31:	30:	29:	28:	27:	26:	25:	24:
	EEEEG	ABB28750	RRRRR	RRRRR	RRRRR	RRRRR	KRRRR	KKRRR	KKKRR	KKKKR	RKKKK	KRKKK	KKRKK	KKKRK	KKKKR	KKKKK	RKKKK	KRKKK	KKRKK	KKKRK	KKKKR	XXXXX	KKKKK	RKKKK
(R,K)[20]	(R,K)[20] (R,K)[20] RRRKKKRKKKKKKKKKKK KKKKK	ck: 1334 len: 86   Abb28750 Peptide #1401 encoded by breas	(R)[20] RRRRRRRRRRRRRRRRRRR NKOTK	(R)(20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RRERERERERERERERERERERERERERERERERERER	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K)(20) KRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K)(20) KKRRRRRRRRRRRRRRRR RRRRR	(R,K)(20) KKKRRRRRRRRRRRRRRR RRRRR	(R,K)[20] KKKKRRRRRRRRRRRRRR RRRRR	(R,K){20} RKKKKRRRRRRRRRRRRR RRRRR	(R,K)(20). KRKKKKRRRRRRRRRRRR RRRRR	(R,K){20} KKRKKKRRRRRRRRRRR RRRRR	(R,K)(20) KKKKKKKRRRRRRRRRRR RRRRR	(R,K)(20) KKKKKKKKRRRRRRRRRR RRRRR	(R,K)(20) KKKKKKKKKKRRRRRRRRR RRRRR	(R,K)[20] RKKKKRKKKKRRRRRRRRR RRRRR	(R,K)[20] KRKKKKKKKKKBRRRRRR RRRRR	KKRKKKKKKKKKRRRRRRR RRRRR

44: RKERR	43: GRKER	42: EGRKE	ABB29645	49: EEKKK	48: EEEKK	47: KEEEK	46: KKEEE	23: EEEEE	АВВ29360	35: GRGRR	34: EGRGR	33: EEGRG	ABB28840	67: KKRKR	66: KKKRK	65: KKKKR	64: RKKKK	63: RRKKK	62: RRRKK	61: GRRRK	60: EGRRR	59: EEGRR
(R,K){20} RRRRRRRRRRRRRRRKRKRR	(R,K){20} RRRRRRRRRRRRRRRKRKR	(R,K)(20) (R,K)(20) RRRRRRRRRRRRRRRRRKRK	ck: 1939 len: 130 !	(R,K){20}	(R,K){20} KKKKKKKKKKKKKKKKKKK	(K) [20]	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (R,K){20} KKKKKKRKRKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 2276 len: 89 !	(R,K)[20] RRRRKRRKRRKRRKRRKRRR	(R,K){20} RRRRRKRRKRRKRRKRRKRR	(R,K)(20) (R,K)(20) RRRRRRRKRRKKRRKRKKR	ck: 9082 len: 167 !	(K){20} KR KKKKKKKKKKKKKKKKKK	(R,K){20}	(R,K){20}	KK RKRKKKKKKKKKKKKKKK KKK	(R,K){20}	(R, K) {20} KKRKRKKKKKKKKKKKKKKKK	(R,K){20} KKKRKRKKKKKKKKKKKKKKK	(R,K){20} KKKKRKRKKKKKKKKKKKKKK	(R,K){20} RR RKKKRRKKKKKKKKKKKK KKKKK
RRRRK	RRRRR.	RRRRR	Abb29645 Peptide #2296 encoded by breas		KEEEE	RKEEE	KRKEE	EEEKK	Abb29360 Peptide #2011 encoded by bre	GGGRR	RGGGR	RRGGG	Abb28840 Peptide #1491 encoded by bre				K	KK	KKKKK	KKKKK	KKKKK	ккк
<del></del>	<del></del> ,		est ce						breast ce			1	breast ce									

51:	50:	49:	48:	47:	46:	45:	44:	43:	42:	41:	40:	39:	АВВ:	54:	53:	52:	51:	50:	49:	48:	47:	46:	45:
KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	EKKKK	REKKK	KREKK	RKREK	ERKRE	АВВ29928	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	ERRRR	KERRR
(K){20} KKKKKKKKKKKKKKKKKKK KI	(K){20}	(K)(20) KKKKKKKKKKKKKKKKKK KI	(K){20} KKKKKKKKKKKKKKKKKKKK K!	(K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK K	(K){20} KKKKKKKKKKKKKKKKKKK K	(K){20} KKKKKKKKKKKKKKKKKKK K	(K) (20)	(K)(20) KKKKKKKKKKKKKKKKKKK K	(K){20} KKKKKKKKKKKKKKKKKKK K	(K){20} KKKKKKKKKKKKKKKKKKK K	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKK K	ck: 3607 len: 88 !	(R,K)(20) RRRRKRKRRRRRRKKKKKK E	(R,K){20} RRRRRKRKRKRRRRRKKKKK K	(R,K){20} RRRRRRKRKRRRRRRKKKK K	(R,K){20} RRRRRRRKRKRRRRRRKKK K	(R,K){20} RRRRRRRRKRKRRRRRKK K	(R,K){20} RRRRRRRRRKRKRRRRRK K	(R,K)(20) RRRRRRRRRRKRKRRRRRR K	(R,K){20} RRRRRRRRRRKRKRKRRRR R	(R,K)(20) RRRRRRRRRRRRKRKRKRRR R	(R,K)[20] RRRRRRRRRRRRRKRKRRR R
KKKKK .	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK .	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	Abb29928 Peptide #2579 encoded by breas	EEBEE	KEEEE	KKEEE	KKKEE	KKKKE	KKKKK	KKKKK	RKKKK	RRKKK	RRRKK

```
59:
                                                                                                                                                                                                                                57:
                                                                                                                                           (K){20}
                                                                                                                                                       (K){20}
                                                                                                                                                                                                                                                        ABB30512
                                                                              (K)[20]
                                                                                                      66: KKKKK KKKKKKKKKKKKKKKKK KKK
                                                                                                                               (K)(20)
                                                                                                                                                                                                                                                                     54: KKKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                 5
                         ω
..
                                     2
                                                  1:
                                                                                                                                                                                                       (K){20}
                                                                                                                                                                                                                                | (K) {20}
(K){20}
                         ck: 3937 len: 85
                                    (R,K){20}
(K){20}
KKKKKKKKKKKKKKKKKKKKKK KKKK
                                                                ! Abb30512 Peptide #3163 encoded by breast ce
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(R){20}
                              (R){20}
                                        (R){20}
                                                   (R){20}
                                                             (R){20}
                                                                                                                АВВ32308 ck: 1560 len: 88
                                                                                                                                                                                           (K){20}
                                                                                                                                                                                                     10: KKKKK KKKKKKKKKKKKKKKKKKK KEEEE
                                                                                                                                                                                                                         7: KRKKK KKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                              | Abb32308 Peptide #4959 encoded by breat
```

34:	33:	32:	31:	30:	29:	28:	27:	26:	25:	24:	23:	22:	21:	20:	19:	18:	17:	16:	15:	АВВ	62:	61:	60:
KKKRK	KKKKR	KKKKK	RKKKK	KRKKK	KKRKK	KKKRK	KKKKR	XXXXX	KKKKK	RKKKK	RRKKK	RRRKK	RRRRK	RRRRR	GRRRR	RGRRR	RRGRR	RRRGR	RRRRG	33064	RRRRR	RRRRR	RRRRR
(R,K){20} KKKRRRRRRRRRRRRRRRRRR	(R,K){20} KKKKRRRRRRRRRRRRRRRRR	(R,K){20} RKKKKRRRRRRRRRRRRRR	(R,K){20} KRKKKKRRRRRRRRRRRRRR	(R,K){20} KKRKKKKRRRRRRRRRRRR	(R,K){20} KKKRKKKRRRRRRRRRRR	(R,K){20} KKKKRKKKRRRRRRRRRRR	(R,K){20} KKKKKRKKKKRRRRRRRRR	(R,K){20} RKKKKKRKKKKRRRRRRRRR	(R,K){20} KRKKKKKRKKKKRRRRRRR	(R,K){20} KKRKKKKKRKKKKRRRRRRR	(R, K) { 20 } KKKRKKKKKKKKKKKRRRRR	(R, K){20} KKKKRKKKKKKKKKKKRRRR	(R,K){20} KKKKKRKKKKKRKKKRRRR	(R,K){20} KKKKKKKKKKKKKKKKKRRR	(R,K){20} RKKKKKKRKKKKKKKKKKRR	(R, K) {20} RRKKKKKKRKKKKKKKKKKKK	(R,K)[20] RRRKKKKKKKKKKKKKKKKK	(R,K){20} RRRRKKKKKKKRKKKKKKKKK	(R,K){20} (R,K){20} RRRRKKKKKKRKKKKKKKKK	ck: 5383 len: 86	(R) {20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R) [20] RRRRRRRRRRRRRRRRRRRR
RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRR	RRRRR	RRRRR	KRRRR	KKRRR	! Abb33064 Peptide #570 encoded by human fo	NTNNE	RNTNN	RRNTN

```
(R, K){20}
                      ABB33937 ck: 1334 len: 86
                                                                   (R){20}
                                                                        (R){20}
                                                                                                         (R){20}
                                                                                                               ! Abb33937 Peptide #1443 encoded by human
```

ABB34024 ck: 9082 len: 167

! Abb34024 Peptide #1530 encoded by human

																			٠		
53: 54:	52:	51:	50:	49:	48:	47:	46:	<b>4</b> 5:	44:	43:	42:	ABB	49:	48:	47:	46:	23:	ABB	35:	34:	33:
RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	ERRRR	KERRR	RKERR	GRKER	EGRKE	34819	EEKKK	EEEKK	KEEEK	KKEEE	EEEEE	АВВ34533	GRGRR	EGRGR	EEGRG
(R,K) (20) RRRRRKRKRRRRRRKKKKK (R,K) (20) RRRRRKRKRRRRRKKKKKK	(R,K)[20] RRRRRRKKKRRRRRKKKK	(R,K)[20] RRRRRRRKRKRRRRRKKK	(R,K){20} RRRRRRRRKRKRRRRRRKK	(R,K)[20] RRRRRRRRRKRKRKRRRRKK	(R,K){20} RRRRRRRRRRKRKRKRRRRR	(R,K){20} RRRRRRRRRRRRKKKKRRRR	(R,K)[20] RRRRRRRRRRRRKRKRKRRR	(R,K){20} RRRRRRRRRRRRRKRKRRR	(R,K){20} RRRRRRRRRRRRRRRKRKRR	(R,K){20} RRRRRRRRRRRRRRRRKRKR	(R,K)(20) (R,K)(20) RRRRRRRRRRRRRRRRRKRK	ck: 1939 len: 130	(R,K){20}	(R,K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(R,K)(20) (R,K)(20) KKKKKKRKRKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 2276 len: 89	(R,K){20} RRRRRKRRRKRRKRRKRRR	(R,K){20} RRRRRKRRKKRRKRRKRR	(R,K)(20) (R,K)(20) RRRRRRKRRKKRRKKRKKR
KEEEE	KKEEE	KKKEE	XXXXE	XXXXX	KKKKK	RKKKK	RRKKK	RRRKK	RRRRK	RRRRR	RRRRR	i Abb34819 Peptide #2325 encoded by human foe	EEEEE	KEEEE	RKEEE	KRKEE	EEEKK	! Abb34533 Peptide #2039 encoded by human foe	GGGRR	RGGGR	RRGGG

61:	60:	59:	58:	57:	56:	55:	54:	53:	52:	51:	50:	49:	48:	47:	46:	45:	44:	43:	42:	41:	40:	39:	ABB:
KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	EKKKK	REKKK	KREKK	RKREK	ERKRE	АВВ35110
(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K)[20] KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20}  KKKKKKKKKKKKKKKKKKKKK	ck: 3607 len: 88									
KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	! Abb35110 Peptide #2616 encoded by human

22:	21:	20:	АВВ	11:	10:	9:	8:	7:	6.	5:	4.	ω 	2:	1:	ABB35	69:	68:	67 :	66:	65:	64 :	63:	62:
KKQKK	KKKQK	KKKKQ	36406	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKK	KKK	KK	<b>7</b>		35676	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKK	ck: 2686 len: 71	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKK	ck: 3937 len: 85	(K){20}	(K) (20)	(K) (20)	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK
KKRKR	KKKRK	KKKKR	Abb36406 Peptide #3912 encoded by human foe	EEEEX	KEEEE	KKEEE	KKKEE	KKKKE	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	! Abb35676 Peptide #3182 encoded by human foo		*	KK	KKK	KKKK	KKKKK	KKKKK	KKKKK

46:	45:	44:	43:	42:	41:	40:	39:	38:	37:	36:	35:	34:	3 3 :	32:	31:	30:	29:	28:	27:	26:	25:	24:	23:
KKKRK	KKKKR	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	OKKKK	KQKKK
(R,K)(20) RKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)(20)	RKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)[20]	(R,K){20}	(R,K){20}	(R,K){20}	(R,K){20}	(R,K){20}	(R,K)(20)	(R,K){20}	(R,K){20}	(R,K){20} KKKKKKKKKKKKKKKKKR	(K){20}	(K)(20) KKKKKKKKKKKKKKKKKKKKK									
KKKSA	KKKKS	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXX	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXX	XXXXX	RKKKK	KRKKK	RKRKK	KRKRK

62:	61:	60:	59:	5 <b>8</b> :	57:	56:	55:	54:	53:	52:	51:	50:	49:	48:	47:	46:	45:	44:	43:	АВВ	49:	48:	47:
RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	GRRRR	RGRRR	RRGRR	ERRGR	RERRG	ABB37567	RKRKK	KRKRK	KKRKR
(R){20} RRRHRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRR	(R,K){20} (R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 1560 len: 88	(K)[20] KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK
NTNNE	RNTNN	RRNTN	RRRNT	RRRRN	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRR	RRRRR	RRRRR .	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	! Abb37567 Peptide #5073 encoded by human for	SAH	KSAH	KKSAH
	1					<b>-</b>	i							<b>L</b>					-			1	

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(R,K){20}
19: FKPMR KRRRKKKRRRKKRKKKRRK KLTTT
                                  (R,K){20}
(R,K){20}
18: LFKPM RKRRRKKKRRRKKKKKKKRR KKLTT
                                                                                       ABB44317 ck: 4895 len: 51
                                                                                                                                                                                                                                                                                                                                                                     ABB42642 ck: 2394 len: 57 ! Abb42642 Peptide #10148 encoded by huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (R,K)[20]
(R,K)[20]
16: KERKT KKRKRKRRRRKKRR R
                                                                                                                                                                                                                                          1.
                                                                                                                                                                                                                                                                                           ABB43181 ck: 4228 len: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB40272 ck: 8343 len: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (R,K){20}
17: ERKTK KRKRKRRRRKKRRRKKRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB37780 ck: 2324 len: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9: REKKK KRKKKKKKKKKKKKKKKKK NKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8: EREKK KKRKKKKKKKKKKKKKKK KNKKK
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RRR RRRRKKKKRRRRRRRRRRRKR T
                                                                                                                                                                 (R,K)[20]
RR RRRRRKKKKRRRRRRRRRR RT
                                                                                                                                                                                                     (R,K)[20]
RRRRRRKKKKRRRRRRRRRR KRT
                                                                                                                                                                                                                                       (R,K)[20]
(R,K)[20]
RRRRRRKKKKKRRRRRRRRR RKRT
                                                                                                                                                                                                                                                                                         ! Abb43181 Peptide #10687 encoded by huma
                                                                                     ! Abb44317 Peptide #11823 encoded by huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Abb37780 Peptide #5286 encoded by humar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ! Abb40272 Peptide #7778 encoded by humar
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	32:	31:	30:	29:	28:	27:	26:	25:	24:	23:	22:	21:	20:	19:	18:	17:	16:	15:	ABB1	22:	21:	ABB1	20:
	KKKKK	RKKKK	KRKKK	KKRKK	KKKRK	KKKKR	KKKKK	XXXXX	RKKKK	RRKKK	RRRKK	RRRRK	RRRRR	GRRRR	RGRRR	RRGRR	RRRGR	RRRRG	18534	FTTEK	FFTTE	17165	KPMRK
(R,K){20}	(R,K){20} RKKKKRRRRRRRRRRRRRRRR	(R,K){20} KRKKKKRRRRRRRRRRRRRRR	(R,K){20} KKRKKKKRRRRRRRRRRRR	(R,K){20} KKKRKKKKRRRRRRRRRRR	(R,K){20} KKKKRKKKRRRRRRRRRR	(R,K){20} KKKKKRKKKRRRRRRRRR	(R,K){20} RKKKKKRKKKKRRRRRRRR	(R,K){20} KRKKKKKRKKKKRRRRRRR	(R,K){20} KKRKKKKKRKKKKRRRRRR	(R, K) {20} KKKRKKKKKKKKKKRRRRRR	(R,K){20} KKKKRKKKKKKKKKKRRRR	(R,K){20} KKKKKRKKKKKRKKKKRRRR	(R, K) {20} KKKKKKRKKKKKRKKKRRR	(R, K) {20} RKKKKKKRKKKKKKKKKRR	(R, K) (20) RRKKKKKKRKKKKKKKKKK	(R,K){20} RRRKKKKKKRKKKKKKKKKK	(R,K){20} RRRRKKKKKKKKKKKKKKKKKK	(R,K){20} (R,K){20} RRRRRKKKKKKKKKKKKKKKK	ck: 5383 len: 86	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 8887 len: 42	(R,K){20} RRRKKKRRRKKRKKKRRRKK
	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR .	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	KRRRR	KKRRR	Abb18534 Protein #533 encoded by probe for	×	KX X	Abb17165 Human nervous system related polyp	LTTT

	66:	65:	64:	63:	62:	61:	60:	59:	58:	57 :	АВВ:	45:	44:	43:	42:	41:	40:	39:	38:	37:	36:	35:	34:	33:
	KKKRK	KKKKR	RKKKK	RRKKK	RRRKK	GRRRK	EGRRR	EEGRR	EEEGR	EEEEG	ABB19373	RRRRR	RRRRR	RRRRR	RRRRR	KRRRR	KKRRR	KKKRR	KKKKR	RKKKK	KRKKK	KKRKK	KKKRK	KKKKR
(K)(20)	(R,K){20}	(R,K){20} KRKKKKKKKKKKKKKKKK KK	RKRKKKKKKKKKKKKKK KKK	KRKRKKKKKKKKKKKKK KKKK	(R,K){20} KKRKRKKKKKKKKKKKK KKKKK	KKKRRRKKKKKKKKKKKK KKKKK	KKKKRKRKKKKKKKKKKK KKKKK	RKKKRRKRKKKKKKKKKK KKKKK	(R,K)[20] RRKKKKKKKKKKKKKKKKK KKKKK	(R,K)[20] (R,K)[20] RRRKKKRKKKKKKKKKKK KKKKK	ck: 1334 len: 86 ! Abb19373 Protein #1372 encoded by probe	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) RRERERERERERERERE RERNK	(R){20} RRRRRRRRRRRRRRRRRR RRRN	(R)(20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRHRHRRRRRRRRRRRRRR RRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K)[20] KRRERRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K)[20] KKRRRRRRRRRRRRRRRRR RRRRR	(R,K)[20] KKKRRRRRRRRRRRRRRRR RRRRR	KKKRRRRRRRRRRRRRRR RRRRR

(R,K){20} 53: RRRRR RRRRRKKKKRKRRRRRKKKKK KEEEE	(R,K)[20] 52: RRRRR RRRRRRKRKRKRRRRRKKKK KKEEE	(R,K){20} 51: RRRRR RRRRRRRKKKKRRRRRRKKK KKKEE	(R.K){20} 50: RRRRR RRRRRRRRRKRKRRRRRKK KKKKE	(R,K){20} 49: RRRRR RRRRRRRRRRKRKRRRRRRK KKKKK	(R,K)[20] 48: RRRRR RRRRRRRRRRKRRRRRR KKKKK	(R,K){20} 47: RRRRR RRRRRRRRRRRRKRKRRRRR RKKKK	(R,K){20} 46: ERRRR RRRRRRRRRRRRRKRKRRRR RRKKK	(R,K)[20] 45: KERRR RRRRRRRRRRRRRKRKRRR RRRKK	(R,K){20} 44: RKERR RRRRRRRRRRRRRRRRKRKRR RRRRK	(R,K)(20) 43: GRKER RRRRRRRRRRRRRRRRKRKR RRRRR	42: EGRKE RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	1 Abb20238 Protein #2237 encoded by	K KKKKKKKKKKKKKKKKKK EE	48: EEEKK KKKKKKKKKKKKKKKKKKK KEEEE (R,K){20}	KEEEK	KKEEE	93333	. (R,K)(20) (R,K)(20)	19943 ck: 2276 len: 89	(R,K)(20) 35: GRGRR RRRRRKRRKKRRKRRR GGGRR	(R,K)[20] 34: EGRGR RRRRRKRRKRRKRRKRR RGGGR	(R,K){20} (R,K){20} 33: EEGRG RRRRRRKRRKKRRKRRKR RRGGG	ABB19467 ck: 9082 len: 167 ! Abb19467 Protein #1466 encoded by	67: KKRKR KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
(R){20}	(K){20}  S9: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20) 58: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	57: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	56: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20)  55: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK	54: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	-(K)(20) 53: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	52: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	51: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	50: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	49: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	Probe for 48: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(X){20}	46: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	45: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	44: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	43: EKKKK KKKKKKKKKKKKKKKKK KKKKK	(K){20} 42: REKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 41: KREKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	40: RKREK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 39: ERKRE KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ABB20531 ck: 3607 len: 88 ! Abb2( (R,K){20}	by probe for	(R,K){20}

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31 ck: 3607 len: 88 ! Abb20531 Protein #2530 encoded by probe
                                                                                                                                                                                                                                                                                                                           (R,K){20}
RRR RRRRRKKKKKKK EEEEE
                                                        (K){20}
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              (K)(20)
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	••	АВВ2	••	.0:	9:		7:	6:	··	4 .	ω	2:	1:	ABB2	9.		7:	••	5		ω 	2	61:
	KKKKQ	1763	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXX	XXX	××	7	•	1105	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK
(K){20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 2686 len: 71	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KXKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 3937 len: 85	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK
	KKKKR	Abb21763 Protein #3762 encoded by probe for	EEEEX	KEEEE	KKEEE	KKKEE	KKKKE	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	! Abb21105 Protein #3104 encoded by probe for		***	KK	KKK	KKKK	KKKKK	KKKKK	KKKKK	KKKKK

	37: 38: 39: 40: 41:	<b>ω 4 το σ</b>	2 1 0 9	21: 22: 23: 24: 25: 26: 27:
(20)  KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	KKKKK KKKKK KKKKKK KKKKKK KKKKKK KKKKKK		KKKKK  KKKKK	KKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
REMAKE RE	KKKKKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	KRKRKKKKK CRKRKKKKKK XKRKKKKKKK CRKKKKKKKK	(20) KKKKKKKKKKKKKKKK (20) (20) KKKKKKKKKKKKKKKK KKKKKKKKKKKKKKK (20) KKKKKKKKKKKKKKKKK (20)	KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK

	RNTNN	(R)[20] RR RARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	61: RRRRR
ъ	RRNTN	(R){20} RR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	60: RRRRR
	RRRNT	(R){20} RR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	59: RRRRR
	RRRRN	(R){20} RR RRRRRRRRRRRRRRRRRR	58: RRRRR
	RRRRR	(R)[20] RR RRKRRRRRRRRRRRRRRR	57: RRRRR
H	RRRRR	(R){20} RR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	56: RRRRR
•	RRRRR	(R){20} RR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	55: RRRRR
	RRRRR	(R){20} RR RRKRRRRRRRRRRRRRRRR	54: RRRRR
	RRRRR	(R){20} RR RRRRRRRRRRRRRRRRRRRR	53: RRRRR
	RRRRR	(R){20} RR RRRRRRRRRRRRRRRRRRR	52: RRRRR
	RRRRR	(R){20} RR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	51: RRRRR
	RRRRR	(R){20} RR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	50: RRRRR
	RRRRR	(R){20} RR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	49: RRRRR
<b>-</b>	RRRRR	(R){20}	48: RRRRR
	RRRRR	(R){20} RR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	47: GRRRR
	RRRRR	(R)[20] RR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	46: RGRRR
	RRRRR	(R)(20) RR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	45: RRGRR
	RRRRR	(R){20} GR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	44: ERRGR
ı	RRRRR	(R,K){20} (R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	43: RERRG
	! Abb22862 Protein #4861 encoded by probe for	2 ck: 1560 len: 88	ABB22862
	SAH	(K){20}	49: RKRKK
<b>L</b>	KSAH	(K){20}	48: KRKRK
	KKSAH	(K){20} KR KKKKKKKKKKKKKKKKKKK	47: KKRKR
	KKKSA	(R,K){20}	46: KKKRK

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ABB10296 ck: 3983 len: 292 ! Abb10296 Human cDNA SEQ ID NO: 604. 1/:
                                                                       (R,K){20}
20: KPMRK RRRKKKRRKKKRKKKKRRKK LTTTT
                                                                                                                                     (R,K){20}
(R,K){20}
18: LFKPM RKRRRKKKRRKKKKKKKRRR KKLTT
                                                                                                                                                                               ABB27176 ck: 4895 len: 51
                                                                                                                                                                                                                                                                                                                                            (R,K){20}
19: FKPMR KRRRKKKRRKKKRKKKRRKK KLTTT
                                                                                                                                                                                                              ABB25988 ck: 2394 len: 57 ! Abb25988 Protein #7987 encoded by prob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (R,K)[20]
(R,K)[20]
16: KERKT KKRKRKRRRKKRRRKKRR R
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17: ERKTK KRKRKRRRRKKRRRKKRRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ! Abb27176 Protein #9175 encoded by prob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ! Abb23064 Protein #5063 encoded by prob
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ABB10485 ck: 7611 len: 315

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(K){20}
274: VEAPR KKKKKKKKKKKKKKKKKKKKK GGRSR
                                                                            3:
                                                                                                        42:
                                                                                                                                   41:
                                                                                                                                                               40:
                   AAU22374 ck: 8278 len: 53
                                                                                                                                                                                                                                               39:
                                                                                                                                                                                                                    38: PSRAK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                     AAU22186
                                                                                                                                                                                                                                                                                                                 15:
                                                                                                                                                                                                                                                                                                                                           (K){20}
                                                                                                                                                                                                                                                                                                                                                                         13:
                                                                                                                                                                                                                                                                                                                                                                                                   (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                              (K)(20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU22148 ck: 4665 len: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36: MTTSK KKKKKKKKKKKKKKKKKKKK XGKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU21948 ck: 444
                                                                         (K){20}
                                                                                                     (K){20}
                                                                                                                                  AKKKK KKKKKKKKKKKKKKKKKKK KKKXK
                                                                                                                                                             (K){20}
SRAKK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                (K){20}
                                              (K)(20)
KKKKKKKKKKKKKKKKKKK XKKIK
                                                                                                                                                                                                                                                                                      ck: 269
(R,K)(20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           len: 66
                                                                                                                                                                                                                                                                                      len: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ! Abb10485 Human cDNA SEQ ID NO: 793, 1/2002
              ! Aau22374 Human cardiovascular system antige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ! Aau22148 Human cardiovascular system antige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! Aau21948 Human cardiovascular system antige
                                                                                                                                                                                                                                                                                 ! Aau22186 Human cardiovascular system antig
```

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(K){20}
242: AKKKK KKKKKKKKKKKKKKKKKK GRPXX
                                                                                                                                                                                                                                                                                                                                                                                                                               (K){20}
                                                                                                                                                                                                                                                                                                                                                                             (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                     239: FANAK KKKKKKKKKKKKKKKKKKK KKKGR
(R){20}
RRRPR RRRRRRRRRRRRRRRRRRRRRRRRRRRR
                                                                                                                                                                44:
                                                                                                                                                                                                                                                                 (R,K){20}
(R){20}
19: RRRRP RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                                                            AAU31467
                                                                                   (R,K){20}
                                                                                                             46:
                                                                                                                                    (K){20}
                                                                                                                                                                                      42:
                                                                                                                                                                                                                                        (K){20}
                                                                                                                                                                                                                                                                                                    AAU27944 ck: 1121 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU23799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLTRK KKKKKKKKKKKKKKKKKKKKKKKKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (K){20}
LKKKK KKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (K)(20)
ILKKK KKKKKKKKKKKKKKKKKK K
                                                          ck: 4264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 6158 len: 272
                                                                                                                                                                                                                                                                                                                                                                                                                (K) [20]
                                                           len:
                                                           657
                                                                                                                                                                                                                                                                                                    69
                                                         ! Aau31467 Novel human secreted protein #1
                                                                                                                                                                                                                                                                                                  ! Aau27944 Human contig polypeptide sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! Aau23799 Novel human enzyme polypeptide
```

(R) {20}

39:	38:	37:	36:	AAEC	128:	127:	126:	125:	124:	123;	122:	121:	120:	119:	118:	117:	116:	115:	114:	AAU:	23:	22:	21:
SXKKK	SSXKK	WSSXK	XSSWX	AAE09664	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	QKKKK	RQKKK	LROKK	QLRQK	TQLRQ	AAU33348	PRRRR	RPRRR	RRPRR
(	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 1663 len: 87	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K) {20}	(K){20} KXKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) (20) KKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 8085 len: 154	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
KKKKK	KKKKK	KKKKK	KKKKK	! Aae09664 Human pancreatic related protein H	XKKKK	KXKKK	KKXKK	KKKXK	KKKKX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKK	! Aau33348 Human breast cancer protein encode	LGLER	RLGLE	RRLGL

(R,K)[20] 63: KKKKK KKKKKKKKKKKKKKKKKKKK	(K){20} 62: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	61: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	60: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 59: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20}	57: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	56: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 55: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 54: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	53: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 52: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 51: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 50: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20) 49: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20}	47: KKKKK KXKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	46: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 45: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20}	(x){20} 43: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 42: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} 40: XKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
GXPFX	RGXPF	KRGXP	KKRGX	KKKRG	KKKKR	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK

75: 1	AAU18168	57: 1	56: 1	55: 1	54	53:	52: 1	AAU181	14:	13:	12:	11:	10:	9:	AAU1816	61:	аам9	114:	113:	112:	111:	AAM95365
РГССО	8168	KKKKK	LKKKK	LLKKK	ILLKK	IILLK	KIILL	8167	KKKKK	LKKKK	DLKKK	EDLKK	FEDLK	YFEDL	8162	KKXFD	6607	NLKKK	LNCKK	HLNLK	IHLNL	5365
(R,K)(	ck: 86	(K)(2	(K)()	(K) (X	(K){X	(K)(X	(R, K) ( (K) () KKKKK	ck: 91	(K)(	(K)(	(K)(	(K){;	(K){;	(R, K) (K) () KKKKK	ck: 79	(R, K) (K) (X)	ck: 47	(K) ()	(K)(X	(K)(	(R,K) (K)() KKKKK	ck: 50
20) KKK	8659	KKKKK	(KKKK	(KKKK	(KKKK	(KKKK	[20] (KKK	9194	(KKKK	20) (KKK)	20] (KKK	20) (KKK	20) KKK	[20] 20) (KKK)	7907	[20] 20] (KKK)	4751	20) (KKK)	20)	20) (KKK)	[20] 20] (KKK)	5626
XXX	len:	KKK	XXXX	XXXX	KKKK	KKKK	KKKK	len:	KKK	CKKKF	CKKK	(KKK)	(KKK)	(KKK)	len:	(KKK)	len:	(KKK)	(KKK)	(KKK)	(KKK)	len:
(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKK	104	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K)(20) (K)(20) KKKKKKKKKKKKKKKKKKKKK	87	(K) (20) KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKK	39	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	80	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20}	139
XXXX	! Aau18168	XKKKK	KXKKK	KKXKK	KKKXK	KKKKX	KKKKK	! Aau18167	GXAAL	KGXAA	KKGXA	KKKGX	KKKKG	KKKKK	! Aau1816		! Aam96607	XKKKK	KXKKK	KKXKK	KKKXK	! Aam95365
	Novel							Novel							2 Novel		7 Human					5 Human
	human							human							human		reprod					reprod
	DNA-binding							DNA-binding							DNA-bi		reproductive					reproductive
	ıding							nding							binding		system					system
	protein							protein					•		protein		relate					related
	# 		···					#							# '0		ted					ď

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AAU18184 ck: 5691 len: 108 ! Aau18184 Novel human DNA-binding protein
                                                               AAU18179 ck: 5503 len: 50
                                                                                                                                                           36: MIFSK KKKKKKKKKKKKKKKKKKKK XGKKK
                                                                                                                                                                                      AAU18178 ck: 444 len: 66 ! Aau18178 Novel human DNA-binding protein
                                                                                                                                                                                                                                                     AAU18177 ck: 8278 len: 53
                                                                                                                                                                                                                                                                                                                                                                AAU18171 ck: 9398 len: 48 ! Aau18171 Novel human DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80: KKKKK KKKKKKKKKKKKKKKKK XGXPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                              (K){20}
QKK KKKKKKKKKKKKKKKKKKK GGRXR
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (R, K){20}
(K){20}
Q KKKKKKKKKKKKKKKKKKKKK KKGGR
                                                                                                                             ! Aau18179 Novel human DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                  ! Aau18177 Novel human DNA-binding protein
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AAU18204 ck: 6110 len: 61
                                 (K){20}
                                                        (K){20}
43: KKKKK KKKKKKKKKKKKKKKKKK K
                                                                              (K){20}
38: PSRAK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                    AAU18200 ck: 7170 len: 63
                                                                                                                                                                                                                                                                     AAU18192 ck: 6029 len: 63
                                                                                                                                                                                                                                                                                           (K){20}
                                                                                                                                                                                                                                                                                                                                      83: KKKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                     (K)(20)
82: LKKKK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (K)(20)
81: CLKKK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (R,K)[20]
       ! Aau18204 Novel human DNA-binding protein #5
                                                                                                                                                                                                                                                                 ! Aau18192 Novel human DNA-binding protein #3
                                                                                                                                                                                                               ! Aau18200 Novel human DNA-binding protein #4
```

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(K){20}
       (K){20}
                                                        (K){20}
                                                                         AAU18205 ck: 5764 len: 74
                                                                                                                     37: KKKKK KKKKKKKKKKKKKKKKKKK GGGGG
                                                                                                                             34: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKGG
                                                                                                                                     ! Aau18205 Novel human DNA-binding prote:
```

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(\kappa){20}
                                                                                                                                                                                                                                                               42:
                                                                                                                                                                                                                                                                                                                                                                                                                        41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (R,K){20}
(K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44:
                                                                                                                                                                                                                                                                                                                         5.
                                                                                                                                                                                                                                                                                                                                               (K){20}
                                                                                                                                                                                                                                                                                                                                                                        43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (K){20}
                                                                                AAU18238
                                                                                                                                        AAU18237
                                                                                                                                                                                                                                         42:
                                                                                                                                                                                                                                                                                                 AAU18208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU18206
                                               (R,K){20}
(R,K){20}

KKKKKKKKKKKKKKKKKKKKKK G
                                                                                                                                                               (K){20}
VRKKK KKKKKKKKKKKKKKKKKKK GGRFR
                                                                                                                                                                                                                                                                                                                                                                       LEPEK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                               PRVRK KKKKKKKKKKKKKKKKKKKK KKGGR
                                                                                                                                                                                                                                        (K){20}
RPRVR KKKKKKKKKKKKKKKKKKKKKKKKKKKGG
                                                                                                                                                                                                                                                                                                                        (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                       ck: 9217 len: 68
                                                                                ck: 5509 len: 58
                                                                                                                                        ck: 285
                                                                                                                                                                                                                                                                                                 ck: 8162 len:
                                                                                                                                        len: 118
                                                                                                                                                                                                                                                                                                 79
                                                                                                                                     ! Aau18237 Novel human DNA-binding protein #
                                                                            ! Aau18238 Novel human DNA-binding protein #
                                                                                                                                                                                                                                                                                              ! Aau18208 Novel human DNA-binding protein #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ! Aau18206 Novel human DNA-binding protein #!
```

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119: KKKKK KKKKKKKKKKKKKKKKKKKK KKKKX
                                                                                                                   (K){20}
                                                                                                                                        (K){20}
                                                                                                                                                                                                                    (K){20}
                                                                                                                                                           (K){20}
                                                                                                                                                                                                 123: KKKKK KKKKKKKKKKKKKKKKKK XXAVL
                                      (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                       AAU18241 ck: 7676
                                                                                                                                                                                                                                                                                    (K)[20]
                                                                                                                                                                                                                                                                                                         45:
                                                                                                                                                                                                                                                                                                                           (K){20}
                                                                                                                                                                                                                                                                                                                                                                 (K){20}
                                                                                                                                                                                                                                                                                                                                                                                     (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU18240 ck: 8528 len: 150 ! Aau18240 Novel human DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU18239 ck: 9074 len: 66
                                                                                                                                                                                                                                                                  len:
 156
! Aau18241 Novel human DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  ! Aau18239 Novel human DNA-binding protein
```

108: KTTWI KKKKKKKKKKKKKKKKKKKK KKKKK

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(R,K){20}
                                                                                                                                                                                                                                                                                                                 (K){20}
                                                                                                                                                                                                                                                                                                                                   (K){20}
                                                   (K){20}
59: KKKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                            (K)(20)
112: IKKKK KKKKKKKKKKKKKKKKKKK KKRGX
                                                                                                                                                                                                                                                                                                                                                                     (K)[20]
110: TWIKK KKKKKKKKKKKKKKKKKKKK KKKKR
                                                                      (K)(20)
57: TKKKK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                         AAU18244 ck: 1109 len: 98
                                                                                                                                                                                                     AAU18242 ck: 1736 len: 40
                                                                                                                                                                                 ! Aau18244 Novel human DNA-binding protein
                                                                                                                                                                                                                                                                            ! Aau18242 Novel human DNA-binding protein #8
```

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AAU18247 ck: 8102 len: 111
                     (K){20}
91: KKKKK KKKKKKKKKKKKKKKKKKKK K
                                                             (K)(20)
                                                                                (K){20}
87: KKKKK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                        (K){20}
                                                                                                                                                            (K){20}
84: KKKKK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                  (K)(20)
79: FHILK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                 AAU18246 ck: 8102
                                                                                                                                                                                                                                                                                                                                              (K){20}
                                                                                                                                                                                                                                                                                                                                                                  (K){20}
KKKKK KKKKKKKKKKKKKKKKKKK KKKK
                                                                                                                                                                                                                                                                                                                         len: 111 ! Aau18246 Novel human DNA-binding prote
! Aau18247 Novel human DNA-binding protei
```

21:	20:	19:	18:	17:	16:	15:	14:	13:	AAU!	92:	91:	90:	89:	88 :	87:	86:	85:	84:	83:	82:	81:	80:	79:
KKKKK	XXXXX	KKKKK	KKKKK	PKKKK	KPKKK	FKPKK	YFKPK	RYFKP	AAU18248	XXXXX	KKKKK	KKKKK	KXKKK	KKKKK	KKKKK	KKKKK	****	XXXXX	XXXXX	LKKKK	I LKKK	HILKK	F.H.I.LK
(K){20}	(K){20}	(K)[20]	(K){20}	(K)(20)	(K){20}	(K)(20) KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 8319 len: 53	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) (20) KKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) (20) KKKKKKKKKKKKKKKKKKKK	(K) [20] KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) [20] KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKKK KKKKK
KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	! Aau18248 Novel human DNA-binding protein #9	-		KK	KKK	KKKK	KKKKK	KKKKK	XXXXX	KKKKK	XXXXX	XXXXX	XXXXX	XXXXX	KKKKK
					<b>ب</b> سو								н										

						,															٠		
	12:	11:	10:	9:	œ ::	AAU	56:	55:	54:	53:	52:	51:	50:	AAU	30:	29:	28:	27 :	26:	25:	24:	23:	22:
	FKKKK	FFKKK	CFFKK	YCFFK	FYCFF	AAU18252	KKKKK	KKKKK	VKKKK	TVKKK	LTVKK	VLTVK	NVLTV	AAU18250	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
(K){20}	(K){20}	(K)[20] KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKK	ck: 4882 len: 41	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20}	ck: 7918 len: 80	(K){20} KKKKKKKKKKKKKKKKKKK :	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK
	KKKKK	KKKK	KKKKK	KKKKK	KKKKK	! Aau18252 Novel human DNA-binding proteir	XXKKK	KXXKK	KKXXK	KKKXX	KKKKX	KKKKK	KKKKK	! Aau18250 Novel human DNA-binding proteir	XEGX	KXEGX	KKXEG	KKKXE	KKKKX	KKKKK	KKKKK	KKKKK	· KKKKK

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AAU18254 ck: 5075
                                       (K){20}
42: KKKKK KKKKKKKKKKKKKKKKKK XG
                                                      (K)(20)
41: KKKKK KKKKKKKKKKKKKKKKKK KXG
                                                                        (K){20}
                                                                                        (K)[20]
39: KKKKK KKKKKKKKKKKKKKKKKKK KKKXG
                                                                                                         (R) (20)
                                                                                                                         33: LLKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                          (K) [20]
                                                                                                                                                                                                                                                                                 AAU18253 ck: 5469 len: 63
                                                                                                                                                                                                                                                                                                                                                                                len:
                       52
                   ! Aau18254 Novel human DNA-binding protein #1
                                                                                                                                                                                                                                                             ! Aau18253 Novel human DNA-binding protein #1
```

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(K)(20)
                          (K){20}
                                                                                                                        AAU18256 ck: 2868 len: 84
                                                                                                                                                        (K){20}
27: KKKKK KKKKKKKKKKKKKKKKK X
                                                                                                                                                                    (K){20}
                                                                                                                                                                                               (K){20}
22: TTFKK KKKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                       AAU18255 ck: 5741 len: 47
                                                                                                                                                                                                                                                                                                (K){20}
                                                                                                                                                                                                                  (K) (20)
                                                                                                                                         ! Aau18256 Novel human DNA-binding prote
                                                                                                                                                                                                                                                                    ! Aau18255 Novel human DNA-binding prote
```

AAU18257 ck: 4686 len: 73

! Aau18257 Novel human DNA-binding protei

```
50:
                                                                                                   49:
                         AAU18259
                                                                                                                      48:
                                                                                                                                                                                                   (K){20}
                                                                                                                                                                                                                                        50:
                                                                                                                                                                                                                                                                             49:
                                                                                                                                                                                                                                                                                              (K){20}
                                                                                                                                                               AAU18258 ck: 6676 len: 74
                                                                                                                                                                                                                                                                                                                 (K){20}
                                                                                                                                                                                                                                                                                                                                   (K){20}
                                                                                                                                                                                                                                                                                                                                                                       (K){20}
                                                                                                                                                                                                                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                             (K){20}
                                           (K)(20)
KKKKK KKKKKKKKKKKKKKKKKK XXG
                                                            (K){20}
QKKKK KKKKKKKKKKKKKKKKKKK KXXG
                                                                               (K){20}
RTFQK KKKKKKKKKKKKKKKKKKKK KKKKX
                                                                                                 (K)(20)
TFQKK KKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                     (K)(20)
                         ck: 2283
       (R,K){20}
(K){20}
                         len: 54
                                                                                                                                                             ! Aau18258 Novel human DNA-binding protein #
                     ! Aau18259 Novel human DNA-binding protein #
```

```
(K)(20)
11: KKKKK KKKKKKKKKKKKKKKKK X
                    AAU18262 ck: 5199 len: 84
                                                                                                                                                                                                         (K){20}
                                                                                                                                                                                                                                                                                                                (K){20}
                                                                                                                                                                                                                                                                                                                                      (K){20}
                                                                                                                                                                                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                                                                                                                                                               (K){20}
                                                             (R,K){20}
(K){20}
(K){20}
                                                                                                                                     AAU18263 ck: 7578 len: 31
                                                                                                                                                                                                                                                                                                                                                                                                    (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU18260 ck: 7503 len: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (K){20}
34: FCFKK KKKKKKKKKKKKKKKKKKK X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (K)[20]
LEKKK KKKKKKKKKKKKKKKKKK KKX
                                                                                                                                   ! Aau18263 Novel human DNA-binding protein
                                                                                                                                                                                   ! Aau18262 Novel human DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ! Aau18260 Novel human DNA-binding protein
```

	31:	30:	29:	28;	AAU:	176:	175:	174:	173:	172:	171:	170:	169:	AAU	17:	16:	15:	AAU	34:	3 3 :-	32:	31:	AAU
	FHKKK	TFHKK	KTFHK	DKTFH	AAU18267	KKKKK	KKKKK	KKKKK	EKKKK	FEKKK	XFEKK	VXFEK	FVXFE	AAU18266	PLTKK	SPLTK	ISPLT	AAU18265	LLKKK	LLLKK	QLLLK	KQLLL	AAU18264
(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 4672 len: 57	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKK	ck: 657 len: 196	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKK	ck: 3679 len: 37	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20}	ck: 3915 len: 57
	KXPGG	KKXPG	KKKXP	KKKKX	Aau18267 Novel human DNA-binding protein #1	×	ĸ.	KKX	KKKX	KKKKX	KKKKK	KKKKK	KKKKK	! Aau18266 Novel human DNA-binding protein #1	×	X	KKX	! Aau18265 Novel human DNA-binding protein #1	XCGF	KXGGF	KKXGG	KKKXG	! Aau18264 Novel human DNA-binding protein #1
	٦						ب							,							⊢		

```
AAU18272 ck: 269
                                                      (K){20}
41: WKKKK KKKKKKKKKKKKKKKKKK XGXP
                                                                              (R,K){20}
(K){20}
37: LKYEW KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                             AAU18271 ck: 7810 len: 64 ! Aau18271 Novel human DNA-binding protei
                                                                                                                                                                                                           (K)[20]
                                                                                                                                                                                                                                   (K){20}
                                                                                                                                                                                                                                                                                                                               AAU18270 ck: 4665 len: 34
                                                                                                                                                                                                                                                                                                                                                                                       (R,K){20}
                                                                                                                                                                                                                                                                                                                                                                                                               (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                      (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU18268 ck: 9656 len: 66 ! Aau18268 Novel human DNA-binding protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32: HKKKK KKKKKKKKKKKKKKKKKKKK XPGGG
                                len: 76
                                                                                                                                                                                                                                                                                                                                                              ! Aaul8270 Novel human DNA-binding protei
                             ! Aau18272 Novel human DNA-binding protei
```

(K) [20]

```
(K){20}
                   24:
                                                                                                                                                                                                    22:
                                                                                                                                                                                                                       21:
                                                                                                                                                                                                                                          20:
                                                                                                                                                                                                                                                                                                AAU18274 ck: 1663 len:
                                                                                                                                            25: KKKKK KKKKKKKKKKKKKKKKK X
                                                                                                                                                                                                                                                             19:
                                                                                                                                                                                                                                                                               18:
                                                                                                                                                                                                                                                                                                                          AAU18273
                                                                                                                                                                                                                                                                                                                                            (K){20}
                                                                                                                                                                                                                                                                                                                                                                43:
                                                                                                                                                                                                                                                                                                                                                                                   42:
                                                                                                                                                                                                                                                                                                                                                                                                     41: AKKKK KKKKKKKKKKKKKKKKKK KKKXK
                                                                                                                                                                                                                                                                                                                                                                                                                        40: RAKKK KKKKKKKKKKKKKKKKK KKKKX
                                                                                                                                                                                                                                                                                                                                                                                                                                          39: SRAKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                              (K)[20]
                                                                                                                                                                                                                       (K)[20]
QKKKK KKKKKKKKKKKKKKKKKKKK KKKKX
                                                                                                                                                                                                                                                           (K){20}
                                                                                                                                                                                                                                         TOKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                              (K)(20)
                                                                                                                                                                                                                                                                                                                          ck: 8370 len: 45
                                                                                                                         87
                                                                                                                      ! Aau18274 Novel human DNA-binding protein #:
                                                                                                                                                                                                                                                                                                                        ! Aau18273 Novel human DNA-binding protein #1
```

```
(R,K){20}
63: KKKKK KKKKKKKKKKKKKKKKKKK GXPFX
        62: KKKKK KKKKKKKKKKKKKKKKKK RGXPF
                (K){20}
                                         (K) (20)
                                                                                          (K){20}
                                                                                                  (K){20}
                                                                                                                           (K){20}
                                                                                                                                   (K){20}
                                                                                                                                           (K)(20)
```

AAU18275 ck: 5607 len: 63

1 Aau18275 Novel human DNA-binding protein

```
(K) [20]
                                                                                                 (K){20}
                                                           (K){20}
                                                                              41: FLSAK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                             (K){20}
                                                                                                                                                                (K){20}
                                                                                                                                                                                                                                                                                                                                                   38: KKKKK KKKKKKKKKKKKKKKKKK KKGGP
                                                                                                                                                                                                                                                                                         36: KKKKK KKKKKKKKKKKKKKKKKKK KKKKG
                                                                                                                                                                                                                                                                                                                                                                       32: KKKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                AAU18277 ck: 5764 len: 74
                                                                                                                                                                                           AAU18276 ck: 5997 len: 58
                                                                                                                                                                                                              (K){20}
                     (K)(20)
AKKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                         ! Aau18277 Novel human DNA-binding protein #1
                                                                                                                                                                                        ! Aau18276 Novel human DNA-binding protein #1
```

```
(K){20}
                                                                (R){20}
                                                                                                                          (K) (20)
                                                                                                                                                           (K){20}
                                                                                                                                                                                        (K) (20)
                                                                                                                                                                                                                                (K){20}
                                                                                                                 58: GCSYK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                   (K){20}
                                                                                                                                        AAU18278 ck: 7734 len: 97
                                                                                                                                                                     (K){20}
(K) {20}
                                                                                                                                        ! Aau18278 Novel human DNA-binding protein
```

36:	AAU:	27:	26:	25:	24:	23:	22:	A.A.U	161:	160:	159:	158:	157:	156:	155:	154:	AAU	75:	74:	73:	72:	71:
FTLQT	AAU18281	KKKKK	NKKKK	KNKKK	KKNKK	DKKNK	DDKKN	AAU18280	KKKKK	KKKKK	KKKKK	EKKKK	PEKKK	KPEKK	RKPEK	TRKPE	AAU18279	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
(R,K){20} (R,K){20} RKKKKKKKKKKKKKKKKKKK	ck: 9316 len: 67	(K) (20) KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKK	· (K){20}	(R,K) [20] (K) [20] KKKKKKKKKKKKKKKKKKKKKKK	ck: 7117 len: 55	(K)(20) KKKKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20}	(K){20}	(K){20}	(K){20}	(R,K){20} (K){20}	ck: 3164 len: 181	(K) (20)	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK
KKKKK	! Aau18281	XGGRF	KXGGR	KKXGG	KKKXG	KKKKX	KKKKK	! Aau18280	×	ΚX	KKX	KKKX	KKKKX	KKKKK	KKKKK	KKKKK	! Aau18279	xgx	KXGX	KKXGX	KKKXG	KKKKX
	Novel							Novel									Novel					
	human							human									human					
	DNA-binding							DNA-binding				•					DNA-binding		·			
	protein #							protein #									protein #					

32:	31:	30:	29:	28:	27:	26:	25:	24:	23:	22:	21:	20:	19:	18:	17:	16:	15:	AAM5	41:	40:	39:	38:	37:
KKKKK	RKKKK	KRKKK	KKRKK	KKKRK	KKKKR	KKKKK	KKKKK	RKKKK	RRKKK	RRRKK	RRRRK	RRRRR	GRRRR	RGRRR	RRGRR	RRRGR	RRRRG	53862	RKKKK	TRKKK	QTRKK	LQTRK	TLQTR
(R,K){20} RKKKKRRRRRRRRRRRRRRR	(R,K){20} KRKKKKRRRRRRRRRRRRRRR	(R,K){20} KKRKKKKRRRRRRRRRRRRR	(R,K){20} KKKRKKKKRRRRRRRRRR	(R,K){20} KKKKRKKKKRRRRRRRRRRR	(R,K){20} KKKKKRKKKKRRRRRRRRR	(R,K){20} RKKKKKKKKKKKRRRRRRRR	(R,K){20} KRKKKKKRKKKKRRRRRRRR	(R,K){20} KKRKKKKKKKKKKKRRRRRRR	(R,K){20} KKKRKKKKKKKKKKKRRRRRR	(R, K) {20}	(R,K){20}	(R,K){20} KKKKKKKKKKKKKKKKKRRR	(R,K){20}	(R,K){20} RRKKKKKKKKKKKKKKKKK	(R,K){20}	(R,K){20} RRRRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20} (R,K){20} REFERKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 5383 len: 86	(K){20}	(K){20}	(K){20}	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK
RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	KRRRR	KKRRR	! Aam53862 Human brain expressed single ex	XGGRF	KXGGR	KKXGG	KKKXG	KKKKX

(R,K){20}	(R,K)(20) 65: KKKKR KRKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20}	(R,K){20}	(R,K)(20) 62: RRRKK KKRKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)[20] 61: GRRRK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20} 60: EGRRR KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20} 59: EEGRR RKKKKRKKKKKKKKKKKKK KKKKK	(R,K){20} 58: EEEGR RRKKKKKKKKKKKKKKKKK KKKKK	(R,K)(20) (R,K)(20) 57: EEEEG RRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAM54700 ck: 1334 len: 86 ! Aam54	(R){20} 45: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 44: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 43: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 42: RRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) 41: KRRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] 40: KKRRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 39: KKKRR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 38: KKKKR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} 37: RKKKK RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} 36: KRKKK KRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} 35: KKRKK KKRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} 34: KKKRK KKKRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} 33: KKKKR KKKKRRRRRRRRRRRRRRRRRRRRRRRRRR
										Aam54700 Human brain expressed single exon													
52:	51:	50:	49:	. 4.60	47:	46	45	44:	43:	42:		49	. 48	47:	46	23:	1	۵ ۲.	ىئ دۇمار	, u	1	A.A	67:
: RRRRR	: RRRRR	RRRRR	RRRRR	8: RRRRR	': RRRRR	6: ERRRR	5: KERRR	: RKERR	: GRKER	: EGRKE	AAM55623	9: EEKKK	8: EEEKK	: KEEEK	6: KKEEE	: EEEEE	AAM55320	o: GRGRR				AAM54795	7: KKRKR

```
(R,K)[20]
                                (R,K){20}
RRRRRRRKRKRRRRRRKKKK KKEEE
                                                                                (R,K)(20)
RRRRRRRKRKKKKKKKKKEE
                                                                                                                             (R,K)(20) ~
RRRRRRRRRRKKKKKKKKE
                                                                                                                                                                           (R,K)[20]
REREREREREKEKEREREREK KKKKK
                                                                                                                                                                                                                         (R,K)(20)
RRRRRRRRRRKRKRRRRRR KKKKK
                                                                                                                                                                                                                                                                       (R,K){20}
RRRRRRRRRRRKRKRRRRR RKKKK
                                                                                                                                                                                                                                                                                                                                                                     (R,K)[20]
RRRRRRRRRRRRRRKRKRRR RRRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (R,K)(20)
RRRRRRRRRRRRRRRKRKR RRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (R,K){20}
(R,K){20}
RRRRRRRRRRRRRRRRKRK RRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ck: 1939 len: 130 ! Aam55623 Human brain expressed single e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (R,K)[20]
KKKKKKKKKKKKKKKKKKKK EEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (R,K)(20)
KKKKKKKKKKKKKKKKKKKKK KEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (K) (20)
KKKKKKKKKKKKKKKKKKKK RKEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (K)(20)
KKKKKKKKKKKKKKKKKKKKKKKKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (R,K){20}
(R,K){20}
KKKKKRRKRKKKKKKKKK EEEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ck: 2276 len: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (R,K)[20]
RRRRRKRRRKRRKRRKRRR GGGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (R,K){20}
(R,K){20}
RRRRRRRKRRRKRRKR RRGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ck: 9082 len: 167 ! Aam54795 Human brain expressed single e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (K) {20}
                                                                                                                                                                                                                                                                                                                      (R,K){20}
RRRRRRRRRRRRKRKRRRR RRKKK
                                                                                                                                                                                                                                                                                                                                                                                                                 (R,K)(20)
RRRRRRRRRRRRRRKRKRR RRRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (R,K){20}
RRRRRRKRRRKRRKRRKRR RGGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Aam55320 Human brain expressed single e
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56:
                                                                              54:
                                                                                                                                                                                                                                                               51:
                                                                                                                                    50:
                                                                                                                                                  49:
                                                                                                                                                               48:
                                                                                                                                                                             47:
                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                    43:
                                                                                                                                                                                                                                                                            (K){20}
                                                                                                                                                                                                                                                                                          (R,K){20}
S4: RRRRR RRRRRRRRRRRRRKKKKKK EEEEE
                                                                                                                                                                                                                                                                                                                                         53: RRRRR RRRRRRKRKRKRRRRKKKKK KEEEE
                                                                                                                                                                                                                                                                                                             AAM55931 ck: 3607 len: 88
                                                               (K){20}
                      (K){20}
                                                 (K){20}
                                                                             (K){20}
                                                                                          (K){20}
                                                                                                                     (K)(20)
                                                                                                                                   (K){20}
                                                                                                                                                 (K)[20]
                                                                                                                                                               (K){20}
                                                                                                                                                                            (K){20}
                                                                                                                                                                                                                                   (K) (20)
                                                                                                                                                                                                                                                                                                            ! Aam55931 Human brain expressed single exon
```

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(K){20}
                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                              10: KKKKK KKKKKKKKKKKKKKKKK KEEEE
                                                                                                                                                                (K){20}
                                                                                                                                                                            (K){20}
68: KKKKK KKKKKKKKKKKKKKKKKK K
                                                                                                                                                                                                                                 4.
                                                                                                        ω
                                                                                                                                                   AAM56490 ck: 3937 len: 85
                                                                 2:
                                                    (K){20}
                                                                                          (K)[20]
KKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                        (K) (20)
                                                                                                                     ! Aam56490 Human brain expressed single ex
```

AAM58224 ck: 1560 len: 88

! Aam58224 Human brain expressed single ex

```
(R,K){20}
(R,K){20}
16: KERKT KKRKRKRRRKKRRKKRR R
                                     (R,K){20}
17: ERKTK KRKRKRRRRKKRRRKKRRR
                                                                                           (R){20}
                                                                                                                          (R){20}
                                                                                                                                                                                                                                         (R){20}
                                                                                                                                                                                                                                                                         (R){20}
                                                                                                                                                                                                                                                                                                         AAM61063
                                                                           AAM58395 ck: 2324 len: 36
                                                                                                                                                          (R){20}
                                                                                                                                                                                                                                                          (R){20}
45: RRGRR RRRRRRRRRRRRRRRRR RRRRR
ck: 8343 len: 66
                                                                        ! Aam58395 Human brain expressed single exon
                   ! Aam61063 Human brain expressed single exon
```

```
16: NKKKK KKKKKRKRKRKRKKKKKKK KKKKK
                                                                               14:
                                                                                                                                     (R, K){20}
(R, K){20}
                                                                                                                                                                                                                                                                                                                                                                                                        23:
                                                                                                                                                                                                     AAM64863 ck: 3301 len: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                               22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1:
                                                                                                                                                                                                                                                                                                                                                    AAM64090 ck: 4228 len: 24
                                                                                                                                                                                                                                                                                                                                                                              25: RRRRR RRRRRRRRRRRRRRRRRR GRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM63533 ck: 2394 len: 57
                                                                                                                                                                                                                                 4..
                                                                                                                                                                                                                                                            ω
••
                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9: REKKK KRKKKKKKKKKKKKKKKK NKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (R, K) {20}
KKNKK KKKKKKRKRKRKRKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                  (R,K)(20)
RRR RRRRKKKKRRRRRRRRRRRRR T
                                                                                                                                                                                                                                                           (R,K){20}
RR RRRRKKKKRRRRRRRRRK RT
                                                                                                                                                                                                                                                                                      (R,K)(20)
R RRRRRRKKKKRRRRRRRRRR KRT
                                                                                                                                                                                                                                                                                                               (R,K){20}
(R,K){20}
RRRRRRKKKKRRRRRRRRR RKRT
                                                                                                                                                                                                   ! Aam64863 Human brain expressed single e
                                                                                                                                                                                                                                                                                                                                                  ! Aam64090 Human brain expressed single e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! Aam63533 Human brain expressed single e
```

20:	19:	18:	17:	16:	15:	AAM66	20:	19:	18:	аам6	31:	30:	29:	28:	27:	26:	25:	24:	23:	22:	21:	20:	19:
RRRRR	GRRRR	RGRRR	RRGRR	RRRGR	RRRRG	166249	KPMRK	FKPMR	LFKPM	165355	KRKKK	RKRKK	KRKRK	RKRKR	KRKRK	RKRKR	KRKRK	KKRKR	KKKRK	. KKKKR	KKKKK	KKKKK	· KKKKK
(R,K){20} KKKKKKRKKKKKKKKKKRRR	(R,K){20} RKKKKKKKKKKKKKKKKRR	(R,K){20} RRKKKKKKRKKKKKKKKKR	(R,K){20} RRRKKKKKKKKKKKKKKKKKK	(R, K) {20} RRRRKKKKKKKKKKKKKKKKK	(R,K){20} (R,K){20} RRRRKKKKKKKKKKKKKKKK	ck: 5383 len: 86	(R,K){20} RRRKKKRRRKKRKKKRRRKK	(R,K){20} KRRRKKKRRRKKRKKKRRK	(R,K)(20) (R,K)(20) RKRRRKKKRRRKKRKKRRR	ck: 4895 len: 51	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20}	(R,K){20} KRKKKKKKKKKKKKKKKKKK	(R,K)[20] RKRKKKKKKKKKKKKKKKKKK	(R,K)[20] KRKRKKKKKKKKKKKKKKKKK	(R,K){20}	(R,K){20}	(R,K){20}	(R,K){20} KRKRKRKRKKKKKKKKKKK	(R,K)[20] KKRKRKRKRKKKKKKKKKKKK
RRRRR	RRRRR	RRRRR	RRRRR	KRRRR	KKRRR	! Aam66249 Human bone marrow expressed probe	LTTTT	KLTTT	KKLTT	! Aam65355 Human brain expressed single exon	AF	KAF	KKAF	KKKAF	KKKKA	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK

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44:	43:	42:	41:	40:	39:	38:	37:	36:	35:	34:	33:	32:	31:	30:	29:	28:	27 :	26:	25:	24:	23	22	21
RRRRR	RRRRR	RRRRR	KRRRR	KKRRR	KKKRR	KKKKR	RKKKK	KRKKK	KKRKK	KKKRK	KKKKR	KKKKK	RKKKK	KRKKK	KKRKK	KKKRK	KKKKR	· KKKKK	: KKKK	: RKKKK	: RRKKK	: RRRKK	RRRRK
(R)[20] RRRRRRRRRRRRRRRRRRRR RNKQT	(R){20} RRRRRRRRRRRRRRRRRRRR RRNKQ	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) RRRRRRRRRRRRRRRRRRRRRRRRN	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) RRRRRRRRRRRRRRRRRR RRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} KRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} KKRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} KKKRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} KKKKRERRERRERRERRE REERR	(R,K){20}	(R,K)[20] KRKKKKRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} KKRKKKKRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K)[20] KKKRKKKRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K)[20] KKKKRKKKRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} KKKKKRKKKKRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} RKKKKKRKKKKRRRRRRRRR RRRRR	(R,K){20} KRKKKKKKKKKKKKRRRRRRRR RRRRR	(R,K){20} KKRKKKKRKKKKRRRRRRR RRRRR	(R,K){20} KKKRKKKKKKKKKKKKRRRRR RRRRR	(R,K)(	(R,K)(20)

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49: EEKKK KKKKKKKKKKKKKKKKKKKK EEEEE
                             48: EEEKK KKKKKKKKKKKKKKKKKKK KEEEE
                                                          (K){20}
                                                                                         46: KKEEE KKKKKKKKKKKKKKKKKKK KRKEE
                                                                                                                       (R,K){20}
(R,K){20}
23: EEEEE KKKKKKRKKKKKKKKKKKK EEEKK
                                                                                                                                                                                                                                                           (R,K){20}
(R,K){20}
33: EEGRG RRRRRRKRRKRRKRRKRRKR RRGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35: GRGRR RRRRKKRRKKRRKRRKRRR GGGRR
                                                                                                                                                                                                                              (R,K)[20]
34: EGRGR RRRRRRKRRKRRKRR RGGGR
                                                                                                                                                                                                                                                                                                                                   (R,K){20}
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                                                                                                                                                                 AAM67717 ck: 2276 len: 89
                                                                                                                                                                                                                                                                                                     AAM67180 ck: 9082 len: 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM67100 ck: 1334 len: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (R)(20)
45: RRRRR RRRRRRRRRRRRRRRRR NKQTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Aam67717 Human bone marrow expressed probe
                                                                                                                                                                                                                                                                                                 ! Aam67180 Human bone marrow expressed probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! Aam67100 Human bone marrow expressed probe
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43:
                                                                                                                                              41:
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                                                                                                                                                                                                                                                                          (R,K){20}
S3: RRRRR RRRRRKKKKKKKKKKEEEE
                                                                                                                                                                                                                                                                                                                        (R,K){20}
S1: RRRRR RRRRRRRRKKKKKKKEE
                                                                                                                                                                                                                                                                                                                                                50: RRRRR RRRRRRRRKKKKRRRRRRKK KKKKE
                                                                                                                                                                                                                                                                                                                                                                                                                       47:
                                                                                                                     (K)(20)
                                                                                                                                                                                                                             AAM68298 ck: 3607 len: 88
                                                                                                                                                                                                                                                                                                                                                                         49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (R,K){20}
44: RKERR RRRRRRRRRRRRRRRKRKRR RRRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM68007 ck: 1939 len: 130 ! Aam68007 Human bone marrow expressed pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (K){20}
                                                                                             (R,K){20}
RRRRR RRRRKRKRRRRRKKKKKK EEEEE
                                                                                                                                                                                                                                                                                                 (R,K){20}
RRRRR RRRRRRKKKKKKKKEEE
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(R,K){20}
EGRKE RRRRRRRRRRRRRRRRRRKRK RRRRR
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REFERE REFERENCE KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                      ! Aam68298 Human bone marrow expressed pr
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(K){20}
                                    AAM68869 ck: 3937 len: 85
                                                     (K){20}
                                                              (K){20}
                                                                                      (K){20}
                                                                                               (K){20}
                                                                                                                       (K){20}
                                                                                                               (K)(20)
                                                                                                                                                        (K){20}
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                                                                                                                                                                                         (K){20}
                            (K){20}
! Aam68869 Human bone marrow expressed probe
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5: 6: 7: 7: 9: 9: 9: 11: 11: 11: 20: 20: 21: 21: 22: 22: 23: 23: 23: 24: 25: 25: 26: 27: 28: 29: 29: 29: 29: 29: 29: 29: 20: 20: 20: 20: 20: 20: 20: 20: 20: 20	· * · · ·
5: KKKKK 6: KKKKK 6: KKKKK 6: KKKKK 7: KKKKK 9: KKKKK 9: KKKKK 9: KKKKK 11: KKKKK 11: KKKKK 20: KKKKK 21: KKKKK 22: KKQK 22: KKQK 22: KKKKK 23: KQKKK 23: KKKKK 24: QKKKK 25: KKKKK 26: KKKKK 27: KKKKK 28: KKKKK 28: KKKKK 28: KKKKK 28: KKKKK 28: KKKKKK 28: KKKKKK 29: KKKKKK	
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) (20) KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK

48: RRRRR	47: GRRRR	46: RGRRR	45: RRGRR	44: ERRGR	43: RERRG	AAM70678	49: RKRKK	48: KRKRK	47: KKRKR	46: KKKRK	45: KKKKR	44: KKKKK	43: KKKKK	42: KKKKK	41: KKKKK	40: KKKKK	39: KKKKK	38: KKKKK	37: KKKKK	36: KKKKK	35: KKKKK	34: KKKKK	33: KKKKK
(R){20} R RRRRRRRRRRRRRRRRRR	(R){20} R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} R REFERERERERERERERE	(R){20} R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} R RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} (R){20} G RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 1560 len: 88	(K){20}	(K){20} K KKKKKKKKKKKKKKKKKKK	(K){20}	(R,K){20}	R KRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20}	(R,K){20} K KRKRKKKKKKKKKKKKKK	(R,K){20}	(R,K){20}	(R,K){20}	.(R,K){20}	(R,K){20}	(R,K){20}	(R,K){20}	(R,K){20}	(R,K){20} K KKKKKKKKKKRKKKKKKK	(R,K)[20] K KKKKKKKKKKKKRKKKKKK
RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	! Aam70678 Human bone marrow expressed probe	SAH	KSAH	KKSAH	KKKSA	KKKKS	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
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76347	REKKK	EREKK	TEREK	ETERE	AAM73767	ERKTK	KERKT	ААМ70881	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR
ck: 2394 len: 57	(R,K){20} KRKKKKKKKKKKKKKKKKKK	(R,K){20} KKRKKKKKKKKKKKKKKKKK	(R,K){20} KKKRKKKKKKKKKKKKKKKK	(R,K){20} (R,K){20} KKKKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 8343 len: 66	(R,K){20} KRKRKRRRRKKRRRKKRRR	(R,K){20} (R,K){20} KKRKRKRRRRRKKRRRKKRR	ck: 2324 len: 36	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRR	(R)(20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
! Aam76347	NKKKK	KNKKK	KKNKK	XXXNX	! Aam73767		ਲ	! Aam70881	NTNNE	RNTNN	RRNTN	RRRNT	RRRRN	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR
Human					Human			Human														
bone					bone			bone														
marrow					marrow			marrow			•											
expressed					expressed			expressed														
pr					pr			p														

(R,K){20} (R){20}

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(K){20}
                                                  45:
                                                                                           AAM85748
                                                                                                                        21:
                                                                                                                                                    (K){20}
                                                                                                                                                                                   20: KPMRK RRRKKKRRKKKRKKKRRKK LTTTT
                                                                                                                                                                                                                                                                                                                      (R,K){20}
19: FKPMR KRRRKKKRRRKKKRRKKKRRKKKLTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23:
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                                                                                                                                                                                                                                                           AAM82533
                                                                                                                                                                                                                                                                                                                                                    (R,K){20}
(R,K){20}
18: LFKPM RKRRRKKKRRRKKRRKKKRRR KKLTT
                                                                                                                                                                                                                                                                                                                                                                                            AAM78048 ck: 4895 len: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM76911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1:
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                                                (K)[20]
SLKKK KKKKKKKKKKKKKKKKKKK
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RRR RRRRKKKKRRRRRRRRRRRRR T
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (R,K)[20]
RR RRRRRKKKKRRRRRRRRRRK RT
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R RRRRRRKKKKRRRRRRRRR KRT
                                                                                          ck: 7503 len: 74
                                                                                                                                                                                                                                                          ck: 1736 len: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ck: 4228 len: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (R,K)(20)
(R,K)(20)
RRRRRRKKKKRRRRRRRRR RKRT
(K) {20}
                                                                                                                                                                                                                                                      ! Aam82533 Human immune/haematopoietic antige
                                                                                                                                                                                                                                                                                                                                                                                        ! Aam78048 Human bone marrow expressed probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ! Aam76911 Human bone marrow expressed probe
                                                                                      ! Aam85748 Human immune/haematopoietic antigo
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82: LKKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                      83: KKKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                   (K){20}
                                                                                                          AAM90618 ck: 5691 len: 108 ! Aam90618 Human immune/haematopoietic ant
                                                                                                                                                      52: KKKKK KKKKKKKKKKKKKKKKKK XXG
                                                                                                                                                                       51: QKKKK KKKKKKKKKKKKKKKKKKK KXXG
                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                             (K){20}
                                                                                                                                                                                                                                               (K){20}
                                                                                                                                                                                                                                                                       AAM90546 ck: 6676 len: 74  ! Aam90546 Human immune/haematopoietic ant
                                                                                                                                                                                                                                                                                                            (K){20}
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5 5 3 :	AΑ	92:	91:	90:	89:	88:	87:	86:	85:	84:	83:	82:	81:	80:	79:	78:	AA	89	88	87	86:	85:
: QTKNT	ААМ91162	: KKKKK	: KKKKK	: KKKKK	: KKKKK	· KKKKK	: KKKKK	: KKKKK	: KKKKK	: KKKKK	: KKKKK	: LKKKK	: ILKKK	: HILKK	: FHILK	: EFHIL	ААМ91030	: KKKKK	: KKKKK	: KKKKK	: KKKKK	: KKKKK
(R, K) (20) KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 1109 len: 98	(K) [20] KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKKKK	(R, K) [20] (K) [20] KKKKKKKKKKKKKKKKKKKKKKK	ck: 8102 len: 111	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) {20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK KKKK
KKKKK	! Aam91162 Human immune/haematopoietic antige		K	KK	KKK	KKKK	KKKKK	KKKKK	KKKKK	KKKKX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	! Aam91030 Human immune/haematopoietic antige			KK.	KKK	KKKK

86:	85:	84:	83:	82:	81:	:08	79:	78:	AAM	68:	67:	66:	65:	64:	63:	62:	61:	60:	59:	5. 5.	57:	56:	55:
KKKKK	KKKKK	KKKKK	KKKKK	LKKKK	ILKKK	HILKK	FHILK	EFHIL	аам91891	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	TKKKK	NTKKK	KNTKK
(K){20} KKKKKKKKKKKKKKKKK KKKKK	(K)[20]	(K)[20]	KKKKKKKKKKKKKKKKKK KKKKK	(K){20} KRKKKKKKKKKKKKKKK KKKKK	(K){20} KKKKKKKKKKKKKKKKK KKKKK	(K)(20)	KKKKKKKKKKKKKKKKK KKKK	(R,K)(20) (K)(20) KKKKKKKKKKKKKKKKK KKKKK	ck: 8102 len: 111 ! Aam91891 Human immune/haematopoietic an	(K)[20] KKKKKKKKKKKKKKKKK GGRSR	(K){20} KXKKKKKKKKKKKKKKKK KGGRS	(K)(20) KKKKKKKKKKKKKKKKKK KKGGR	(K)(20) KKKKKKKKKKKKKKKKKK KKKGG	(K)(20) KKKKKKKKKKKKKKKKKK KKKKG	(K)(20) KKKKKKKKKKKKKKKKKK KKKK	(K)(20) KKKKKKKKKKKKKKKKKK KKKK	(K)(20) KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20)	(K)(20)	(K)[20]	(K)[20]	(K)(20)	(K)(20) KKKKKKKKKKKKKKKKK KKKKK

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	48:	47:	46:	45:	44:	43:	42:	41:	40:	39:	38:	37:	36:	AAMS	3 <b>4</b> :	ω 3	AAMS	92:	91:	90:	89:	88 :	87:
	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXKKK	SXKKK	SSXKK	WSSXK	KWSSX	аам92433	PTRPK	PPTRP	ААМ91933	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
(K)[20]	(X)(20)	(K)(20)	(K)(20) KKKKK KKKKKKKKKKKKKKK KKKKK	KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	KKKKK KKKKKKKKKKKKKKKK KKKKK	(K)(20)	KKKKK KKKKKKKKKKKKKKKK KKKKK	KKKKK KKKKKKKKKKKKKKKKK KKKKK	(R) [20]	SXKKK KKKKKKKKKKKKKKKKK KKKKK	SSXKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20)	(R,K)[20] (K)[20] KKKKKKKKKKKKKKKKKK KKKK	ck: 1663 len: 87   Aam92433 Human digestive system antigen SEC	(K){20} KKKKKKKKKKKKKKKKKK GK	(R,K)[20] (K)[20] KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 8285 len: 55 ! Aam91933 Human digestive system antigen SEC	(K){20} KKKKKKKKKKKKKKKKKKKK	(X)(20)	(K)[20]	(K){20}	(K){20}	KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
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AA000232 ck: 1000 len: 102 ! Aao00232 Human polypeptide SEQ ID NO 141
                                                                                         (R,K)[20]
(K)[20]
28: XPLPP KKKKKKKKKKKKKKKKKKKKK GGPPK
                                                                                                                    AA000222 ck: 2916 len: 132 ! Aao00222 Human polypeptide SEQ ID NO 141
                                                                                                                                                              AA0000092 ck: 9065 len: 113 ! Aao00092 Human polypeptide SEQ ID NO 139
                                                                                                                                                                                                                63: KKKKK KKKKKKKKKKKKKKKKKK GXPFX
                                                                                                                                                                                                                                    (K){20}
                                                                                                                                                                                                                                                         (K){20}
                                                                                                                                                                                                                                                                              (K) (20)
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92: LGCLK KKKKKKKKKKKKKKKKKKKKK FF
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55:	54:	53:	52:	51:	50:	49:	48:	47:	46:	45:	44:	43:	42:	41:	40:	39:	38:	37:	36:	35:	34:	33:	32:
KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	XXXXX	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	FKKKK	FFKKK
(K){20} KKKKKKKKKKKKKKKKKKKK	(X){20} KKKKKKKKKKKKKKKKKKKK	(X){20} KXXKXKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20}	(K) (20)	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) {20} KKKKKKKKKKKKKKKKKKKK	(K) {20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) (20)	(K){20} KKKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K) {20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKK
GGPFK	KGGPF	KKGGP	KKKGG	KKKKG	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK

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(R,K){20} 43: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	42: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	41: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	40: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	39: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 38: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	37: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	36: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	35: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	34: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	33: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	32: KKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	31: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	30: KKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20] 29: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	28: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	27: VKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	26: LVKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	25: WLVKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) [20] 24: LMLVK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)[20] (K)[20] 23: CLWLV KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAOO0439 ck: 6396 len: 122 ! AaoO0439 Human polypeptide	(R,K){20} (K){20} 22: OHFCM KKKKKKKKKKKKKKKKKKKKK FFKKG	AAO00291 ck: 8100 len: 124 ! Aao00291 Human polypeptide
•																					olypeptide SEQ ID NO 14		olypeptide SEQ ID NO 14

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(K){20}
                                                                                                                                                                                                        AAO01368 ck: 3955 len: 123 ! Aao01368 Human polypeptide SEQ ID NO 15260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23: LSPEK KKKKKKKKKKKKKKKKKKK SASSS
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(K)(20)
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(K){20}
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                                                                                                                                                                                                                                                            36: KKKKK KKKKKKKKKKKKKKKKKK KTKKK
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(R,K){20}
(K){20}
                                   AAO02733 ck: 2860 len: 132
                                                             89: KKKKK KKKKKKKKKKKKKKKKKKK KKKK
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(R,K){20}
22: HSLNL KKKKKKKKKKKKKKKKKKKKK GGGVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAO02186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ck: 4844 len: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                          len: 137
                              ! Aao02733 Human polypeptide SEQ ID NO 16625
                                                                                                                                                                                                                                                                                                                                                                       ! Aao02477 Human polypeptide SEQ ID NO 16369
                                                                                                                                                                                                                                                                                                                                                                                                                                        ! Aao02310 Human polypeptide SEQ ID NO 16202
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(R,K){20}
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(K){20}
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17: AKARK KKKKKKKKKKKKKKKKKK GGPPL
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                           FAKAR KKKKKKKKKKKKKKKKKKK RGGPP
                                                                                                              (K)(20)
KKKKK KKKKKKKKKKKKKKKKKKK ASSSS
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PKKKK KKKKKKKKKKKKKKKKKKK KKKKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ! Aao02961 Human polypeptide SEQ ID NO 16853
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                                                                                 ! Aao03024 Human polypeptide SEQ ID NO 16916
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AAO03132 ck: 3903 len: 116
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(K){20}
                                                                                ! Aao03132 Human polypeptide SEQ ID NO 170
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(K) [20]

	51: KKKKK	50: KKKKK	49: KKKKK	48: KKKKK	47: LKKKK	46: LLKKK	45: YLLKK	44: XYLLK	43: IXYLL	AA003273	53: HAVKK	52: LHAVK	51: LLHAV	AAO03243	19: СМРКК	18: LLMPK	17: ELLMP	AA003168	14: IXYTR	13: LIXYT	AA003152	6: KKKKK	5: KKKK
(K)(20)	(K){20}	(R,K){20} (K){20}  KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	3 ck: 2981 len: 88	(K){20}	(K){20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	3 ck: 411 len: 95	(R,K){20}	(K){20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	3 ck: 7233 len: 67	(R,K){20}	(R,K){20} (R,K){20}	2 ck: 7891 len: 35	(R,K){20} KK KKKKKKKKKKKKKKKKKKRR	CK KKKKKKKKKKKKKKKKKKK							
	KKKKK	Aao03273 Human polypeptide SEQ ID NO 17165.	EKKRG	KEKKR	KKEKK	! Aao03243 Human polypeptide SEQ ID NO 17135.	GGAPF	RGGAP	KRGGA	! Aao03168 Human polypeptide SEQ ID NO 17060.	ce	RGG	! Aao03152 Human polypeptide SEQ ID NO 17044.	GGPPK	RGGPP								
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27: KKI	26: SKI	25: VSI	24: LV:	23: AL	22: KAI	AAO03284	50: AQ	49: VA	48: AV	47: RA	AAO03278	. 5: <b>X</b>	<b>4</b> -	<b>3</b> :	2:	1:	AA00327	57: KK	56: KK	55: KK	54: KK	53: KK	52: KK
KKKKK	KKKK	VSKKK	LVSKK	ALVSK	KALVS		AQKKK	VAQKK	AVAQK	RAVAQ		KKKK	KKK	XX	*		7	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) (20) KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKK	ck: 9650 len: 115	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(R, K) {20} (K) {20} KKKKKKKKKKKKKKKKKKKKK	ck: 6777 len: 74	(R,K)(20) KKKKKKKKKKKKKKKKKKK	KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 2981 len: 89	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
KRGGA	KKRGG	KKKRG	KKKKR	KKKKK	KKKKK	Aao03284 Human polypeptide SEQ ID NO 17	GGGVL	KGGGV	KKGGG	KKKGG	Aao03278 Human polypeptide SEQ ID NO 17	MKNKK	RMKNK	KRMKN	KKRMK	KKKRM	! Aao03277 Human polypeptide SEQ ID NO 17	PTPKK	KPTPK	KKPTP	KKKPT	KKKKP	KKKKK

(R,K){20} 51: KXKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20} 50: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKXX	(R,K)(20) 49: KKKKK KKKKKKKKKKKKKKKKKKKKKKT	(R,K)(20) 48: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)[20] 47: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	46: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)(20) 45: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	44: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	43: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20] 42: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	41: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	40: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	39: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	38: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	37: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) [20] 36: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20}	34: YPKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	33: SYPKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	32: CSYPK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)(20) (K)(20) 31: SCSYP KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAO03288 ck: 1109 len: 117 ! Aao03288 Human polypeptide SEQ ID NO 17180.	(R,K){20} 29: KKKKK KKKKKKKKKKKKKKKKK GGALK	(K){20} 28: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
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(R, K) {20} (K) {20}	AAO03623 ck: 3884 len: 116 ! Aao03623 Human polypeptide SEQ ID NO 175	(K)(20) 30: PRXKK KKKKKKKKKKKKKKKKK TAAGG	(K)(20) 29: LPRXK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} 28: PLPRX KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAO03615 ck: 7613 len: 128 ! Aao03615 Human polypeptide SEQ ID NO 175	(K){20} 49: KKKKK KKKKKKKKKKKKKKKK GGPRG	(K){20} 48: TKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	47: LTKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) [20] 46: XLTKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20] 45: LXLTK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	44: LLXLT KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)[20]	POLITE ANAMANAMANAMANAMANAMANAMANAMANAMANAMANA	MOVER	. (R,K)[20] (K)[20] 28: XMCVF KKKKKKKKKKKKKKKKK KDPPK	AAO03459 ck: 5217 len: 58   Aao03459 Human polypeptide SEQ ID NO 173	(K)(20) (K)(20)	(K){20} (K){20}	26: XLEEK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)[20] (K)[20] 25: TXLEE KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAOO3375 ck: 693 len: 54   AaoO3375 Human polypeptide SEQ ID NO 172	(R,K){20} 53: KKKKK KKKKKKKKKKKKKKKKK TXGGG	(R,K){20} 52: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK

	AAOO3766 ck: 8808 len: 81 ! AaoO3766 Human polypeptide SEO ID NO 17658		64: KKKKK KKKKKKKKKKKKKKKK KSPGG	63: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	62: EKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	61: AEKKK KKKKKKKKKKKKKKKKK KKKKS	60: DAEKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	59: WDAEK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	58: IWDAE KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK		AAO03703 ck: 7016 len: 113 ! Aao03703 Human polypeptide SEQ ID NO 17595.	(R,K)(20) (K)(20) (K)(20) (K)(20)	AA003700 ck: 1279 len: 43 ! Aa003700 Human polypeptide SEQ ID NO 17592	88: KKKKK KKKKKKKKKKKKKKKK PGGGV	(K) (20) 87: KKKKK KKKKKKKKKKKKKKK KPGGG	86: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	D5: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	84: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	83: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	82: KKKKK KKKKKKKKKKKKKKKKK KKKKK	81: AKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	RAKKK	79: SRAKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) (20) 78: PSRAK KKKKKKKKKKKKKKKKKK KKKKK	77: TPSRA KKKKKKKKKKKKKKKKKKK KKKKK
(K){20}	35: KQNQK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	34: NKONO KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAOO3906 ck: 4312 len: 100 ! AaoO3906 Human polypeptide SEQ ID NO 17	K KKKKKKKKKKKKKKK TKOKK	7777		* * * * * * * * * * * * * * * * * * * *	KKKKK	41: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	40: PKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 39: YPKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	38: HYPKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	37: QHYPK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	1 (R,K)(20) (K){20} 36: KQHYP KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAOO3841 ck: 8734 len: 100 ! AaoO3841 Human polypeptide SEQ ID NO 17	57: KKKKK KKKKKKKKKKKKKKKKKKKKK GGGGA	56: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} 54: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	53: CKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 52: ACKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	51: TACKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	50: TTACK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	49: TTTAC KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	$1 \qquad \qquad (R,K)(20)$

24: KKKKE	AAO04512	25: KKKKK	24: KKKKK	23: KKKKK	22: KKKKK	21: KKKKK	20: SKKKK	19: KSKKK	18: XKSKK	17: LXKSK	16: KLXKS	AA003967	46: KKKKK	45: KKKKK	44: KKKKK	43: KKKKK	42: KKKKK	41: KKKKK	40: KKKKK	39: KKKKK	38: QKKKK	37: NOKKK	36: QNQKK
(R,K)(20) (K)(20) KKKKKKKKKKKKKKKKKKKKK GGGGF	ck: 4277 len: 62	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(R, K) {20} (K) {20}	ck: 7917 len: 53	(K){20}	(x){20}	(K) {20}	(K){20}	ONOKK KKKKKKKKKKKKKKKKKKKK KKKK						
GGGGF	! Aao04512 Human polypeptide SEQ ID NO 18404.	SRGGA	KSRGG	KKSRG	KKKSR	KKKKS	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	Aao03967 Human polypeptide SEQ ID NO 17859.	NGGGG	KNGGG	KKNGG	KKKNG	KKKKN	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
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	XXXXX	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	RKKKK	LRKKK	FLRKK	SFLRK	KSFLR	IKSFL	645	AKPET	644	KKKKK	KKKKK	LKKKK	FLKKK	TELKK	ITFLK	LITFL	619
(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(R,K){20} (R,K){20} RKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 7825 len: 118	(R,K){20} (R,K){20} KKKKKKKKKKKKKKKKKKKK	ck: 2038 len: 70	(K) [20] KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 8654 len: 39
	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	! Aao04645 Human polypeptide SEQ ID NO 185	GGAPL	! Aao04644 Human polypeptide SEO ID NO 185	z	KN	KKN	KKKN	KKKKN	KKKKK	KKKKK	! Aao04619 Human polypeptide SEQ ID NO 185

9 ::	œ .:	AAC	11:	10:	9	AA004	38:	37:	36:	35:	34:	33:	32:	31:	30:	29:	28:	AAC	62:	61:	60:	59:	58:
WFTQK	CWFTQ	AAO04679	YITKK	CYITK	WCYIT	04674	***	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	PKKKK	RPKKK	TRPKK	PTRPK	KPTRP	AAO04647	KKKKK	KKKKK	KKKKK	KKKKK	
(K)(20)	(R,K){20} (K){20} KKKKKKKKKKKKKKKKK KDRG	ck: 7190 len: 31 ! AaoO4679 Human polypeptide SEQ ID NO 18571.	(K)[20] KKKKKKKKKKKKKKKKKK ARG	(K)[20]	(R,K)[20] (K)[20] KKKKKKKKKKKKKKKKKK KKARG	ck: 2036 len: 33   Aao04674 Human polypeptide SEQ ID NO 18566.	(K)(20)	(K)(20)	(K)[20]	(K)(20)	A KKKKKKKKKKKKKKKKKK KKKKS	(K)(20)	A KKKKKKKKKKKKKKKKKKK KKKKK	A KKKKKKKKKKKKKKKKKK KKKK	A KKKKKKKKKKKKKKKKKKK KKKK	(K)(20)	(R,K)[20] (K)[20] KKKKKKKKKKKKKKKKK KKKK	ck: 4805 len: 58 ! Aao04647 Human polypeptide SEQ ID NO 18539.	(K)(20)	(K)(20)	(K)[20] KKKKKKKKKKKKKKKKK KKPRG	(K)(20)	KKKKK KKKKKKKKKKKKKKKKK KKKKP
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(R,K){20}
23: NKLKK KKKKKKKKKKKKKKKKKKKK AAARD
                                                      (K){20}
                                                                                          AAO04743 ck: 9412 len: 54
                                                                                                                                                                                                               AAO04715 ck: 6984 len: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAO04690 ck: 7157 len: 81
                                                                                                                     10: SKDKK KKKKKKKKKKKKKKKKKKKK AKKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAO04682 ck: 5605 len: 60
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LK KKKKKKKKKKKKKKKKKKKK KKQKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ! Aao04682 Human polypeptide SEQ ID NO 18
                                                                                         ! Aao04743 Human polypeptide SEQ ID NO 18
                                                                                                                                                                                                              ! Aao04715 Human polypeptide SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ! Aao04690 Human polypeptide SEQ ID NO 18
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AAO04747 ck: 8399 len: 39

! Aao04747 Human polypeptide SEQ ID NO 18

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37:
                                    36:
                                                      35:
                                                                     (K){20}
34: LEKKK KKKKKKKKKKKKKKKKKKKK KKKKK
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3:
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                                                                                                                                                                      (K){20}
                                                                                                                                                                                        (K){20}
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                                                                                                                                                                                                                                            (K){20}
                                                                                                                                                                                                                                                                22:
                                                                                                                                                                                                                                                                                                  AAO04752 ck: 1021 len: 71
                                                                                                                                                                                                                                                                                                                                                             16: FVKKK KKKKKKKKKKKKKKKKKK GGGF
                                                                                                                                                                                                                                                                                                                                                                                                  (K){20}
                                                                                                                                                                                                                                                                                                                                                                               (K){20}
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                                                     EKKKK KKKKKKKKKKKKKKKKKKK KKKKT
                                                                                                          NSLEK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                               GERKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                     len: 59
                                                                                                                                                                                                                                                                                                                                         ! Aao04752 Human polypeptide SEQ ID NO 18644
                                                                                                                                                 1 Aao04755 Human polypeptide SEQ ID NO 18647
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(K){20}
                 (K){20}
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17: KKKKK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                   (K){20}
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                                                                                                                                                                                                                                                           10: QLKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                             AAO04758 ck: 7836 len: 115
                                                                                                                                                                                                                                                                                                                                                                                                                        AAO04756 ck: 6952 len: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                         9.
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(K){20}
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РООКС	(K) { 20 } KKKKKKKKKKKKKKKKKKK	KKKKK	50:
KPQQK	(K){20} KKKKKKKKKKKKKKKKKKKK	KKKKK	49:
KKPQQ	(K){20}	KKKKK	<b>4</b> 8:
KKKPQ	(K){20}	KKKKK	47:
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KKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	KKKKK	45:
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KKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	KKKKK	43:
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KKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	KKKKK	41:
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	25:	24:	23:	22:	21:	20:	19:	18:	17:	16:	15:	14:	13:	AAC	3 4 :	AAC	14:	13:	12:	11:	10:	9:	AAC
	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	AKKKK	RAKKK	FRAKK	PFRAK	TPFRA	AAO04854	FFSRQ	AAO04802	KKKKK	LKKKK	SLKKK	SSLKK	DSSLK	GDSSL	AA004764
(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 4121 len: 58	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKK	ck: 1223 len: 105	(K) [20] KKKKKKKKKKKKKKKKKKK	(x){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKKK	(R,K) (20) (K) (20) KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 2035 len: 54
	K KKKKK	K KKKKK	K KKKKK	K KKKKK	K KKKKK	K KKKK	K KKKKK	K KKKKK	K KKKKK	CK KKKKK	K KKKKK	CK KKKKK	K KKKKK	! Aao04854 Human polypeptide SEQ ID NO 18	(K GGGGL	! AaoO48O2 Human polypeptide SEQ ID NO 18	K IWEEW	K KIWEF	K KKIWE	KK KKKIW	KK KKKKI	K KKKKK	! Aao04764 Human polypeptide SEQ ID NO 18

26: KKKKK KKKKKKKKKKKKKKKKKKK KKKKK

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53: KKKKK KKKKKKKKKKKKKKKKKKK GGGGP
                                                                                          48:
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                                                                                                                                                                                                                                                                                                                           AAO04872 ck: 3224 len: 93
                                                                                                                                                                                                                                                                                    43:
                                                                                                                                                                                                                                                                                                       42: TLTTK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                              (K){20}
31: KKKKK KKKKKKKKKKKKKKKKKKKK RGGNF
                                                                                                                                                                                                                                                                                                                                                        AAO04856
                                                                                                                                                                                                                                                                                                                                                                                                                                        29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (K){20}
                                                                                                                                                        (R,K){20}
KKKKK KKKKKKKKKKKKKKKKKK GGNFK
                                                                                                                                                                                                                                                                                                                                                                                                                  (K){20}
KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                            (K)(20)
                                                                                                                                                                                                 (K){20}
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                                                                                                                                                                                                                                                                                  (K){20}
                                                                                                                                                                                                                                                                                                                                                       ck: 4861 len: 135
                                             ! Aao04872 Human polypeptide SEQ ID NO 18764
                                                                                                                                                                                                                                                                                                                                                     ! Aao04856 Human polypeptide SEQ ID NO 18748
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31: KKKKK KKKKKKKKKKKKKKKKKKK GGALK
                                      AA004928
                                                                                                  AAO04917 ck: 3999 len: 103
                                                                                                                                                        28: PKKKK KKKKKKKKKKKKKKKKKK KKKGG
                                                                                                                                                                                                                                           (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                  AAO04881 ck: 8841 len: 115 ! Aao04881 Human polypeptide SEQ ID NO 187
                                                                                                                                                                                                                                                                                                                                                                                        (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO04874 ck: 5753 len: 58 / Aao04874 Human polypeptide SEQ ID NO 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAO04873 ck: 7719 len: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12: LKKKK KKKKKKKKKKKKKKKKKK GGPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (K)(20)
FLIEK KKKKKKKKKKKKKKKKKKKKKKK GGGPL
                                      ck: 23
                                                               len: 43
                                                                                                 ! Aao04917 Human polypeptide SEQ ID NO 188
                                   ! Aao04928 Human polypeptide SEQ ID NO 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ! Aao04873 Human polypeptide SEQ ID NO 187
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	12:	11:	:01	9	8.	7:	6.	ა 	AAOC	38:	37:	36:	3 5 :	34:	3 3	32:	31:	30:	29:	28:	27 :	26:	AAO(
	XXXXX	KKKKK	KKKKK	SKKKK	RSKKK	GRSKK	SGRSK	SGRS	AAO05000	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	SKKKK	TSKKK	GTSKK	MGTSK	LMGTS	AAO04969
(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKKK KKKRG	(K){20} KKKKKKKKKKKKKKKKKKK KKKKR	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKK	(K) (20) KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 5847 len: 38	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 4345 len: 57
	KKKRG	KKKKR	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	! Aao05000 Human polypeptide SEQ ID NO 18892.			KK	KKK	KKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK'	KKKKK	! Aao04969 Human polypeptide SEO ID NO 18861.
	٦			<b>-</b>				L				-							<b>1</b>				

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AAO05260 ck: 3618 len: 55
                                                                      (R,K)[20]
(R,K)[20]
30: GYIQL KKKKKKKKKKKKKKKKKKKKKKK GGAFK
                                                                                                              AA005191 ck: 4399 len: 85 ! Aao05191 Human polypeptide SEQ ID NO 19
                                                                                                                                                                                                          AAO05130 ck: 6597 len: 116 ! Aao05130 Human polypeptide SEQ ID NO 19
                                                                                                                                                                                                                                                                                                               (R,K){20}

16: PFQKK KKKKKKKKKKKKKKKKKKKKK GGGFL
                                                                                                                                                                           (K)[20]
15: TPFQK KKKKKKKKKKKKKKKKKKKKK RGGGF
                                                                                                                                                                                                                                                                                 (K)(20)

18: KKKKK KKKKKKKKKKKKKKKKKKKK SSK
                                                                                                                                                                                                                                                                                                                                              (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                          (K){20}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAO05081 ck: 2260 len: 40 ! Aao05081 Human polypeptide SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (R,K){20}
16: KKKKK KKKKKKKKKKKKKKKKKKKKK GGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (K){20}
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(K) (20)

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(K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                    31: KKKKK KKKKKKKKKKKKKKKKKKK GEKKK
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                                                                                                                                                                            (K)[20]
                                                                                                                                                                                                   (K) [20]
                                                                                                                                                                                                                                                  26: TKKKK KKKKKKKKKKKKKKKKKK KKKKR
                                                                                                                                                                                                                                                                         (K){20}
                                                                                                                                                                                                                                                                                               (K){20}
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                                                                                                                                                                                                                                                                                                                                                                                                                             19: QKKKK KKKKKKKKKKKKKKKKKK KKKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17: KHQKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                      AAO05372 ck: 9880 len: 43
                                                                                                                                                                                                                                                                                                                        (K) [20]

(K) [20]
                                                                                                                                                                                                                                                                                                                                                                              AAO05369 ck: 1417 len: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18: HQKKK KKKKKKKKKKKKKKKKK KKKKK
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(K)[20]
KK KKKKKKKKKKKKKKKKKKKK KKKK
                                               ! Aao05372 Human polypeptide SEQ ID NO 19264
                                                                                                                                                                                                                                                                                                                                                                             ! Aao05369 Human polypeptide SEQ ID NO 19261
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(K){20}
             (K){20}
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                                                                                                                                                         17: KKKKK KKKKKKKKKKKKKKKKKKK DSGGG
                                                                                                                                                                      15:
                                                                                                                                                                                                (K){20}
                                                                                                                                                                                                                                                     AAO05499 ck: 7813 len: 76
                                                                                                                                            AAO05384 ck: 715 len: 23
                                                                 (R,K){20}
(K){20}
                                                                                                             ! Aao05499 Human polypeptide SEQ ID NO 19
                                                                                                                                           ! Aao05384 Human polypeptide SEQ ID NO 19:
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7777	,	LKKKK	FLKKK	YFLKK	TYFLK	TTYFL	AA005530	PQSKK	QPQSK	QPQS	AA005500	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	(KKKK	***	KKKK	KKKKK	KKKKK
	(K)(20)	(K) {20}	KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKK KKKKK (K)(20)		(R,K)(20) (K)(20) KKKKKKKKKKKKKKKKK KKKKK	ck: 7354 len: 75 ! Aao05530 Human polypeptide SEQ ID NO 19422	(K){20} KKKKKKKKKKKKKKKKKK ASQKK	(K)[20]	(R,K)(20) (K)(20) KKKKKKKKKKKKKKKKKKK KKASQ	ck: 7443 len: 53   Aao05500 Human polypeptide SEQ ID NO 19392	(K){20} KKKKKKKKKKKKKKKKK ASPGG	(K){20} KKKKKKKKKKKKKKKKK KASPG	KKKKKKKKKKKKKKKKK KKASP	KKKKKKKKKKKKKKKKK KKKAS	(K){20}	(K)(20)	KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20}	KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) (20)	(K) [20]

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	AA006922	34: KKKKK	33: XKKKK	32: MXKKK	31: IMXKK	30: IIMXK	29: VIIMX	AA006429	12: LIKKK	11: CLIKK	10: TCLIK	9: FTCLI	AA006357	32: XKKKK	31: PXKKK	30: LPXKK	29: LLPXK	28: SLLPX	AA006186	7: FLLQK	6: DFLLQ	AA005665
(R,K){20} (K){20}	ck: 7296 len: 111	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) (20)	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 2585 len: 71	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 4679 len: 52	(K){20} KKKKKKKKKKKKKKKKKKKK GGGGF	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) {20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20}  KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 998 len: 88	(R,K)[20] KKKKKKKKKKKKKKKKKKKR	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 432 len: 28
	! Aao06922	GRGGA	KGRGG	KKGRG	KKKGR	KKKKG	KKKKK	! Aao06429	CIKXKK	( KIKXK	C KKIKX	C KKKIK	1 Aao06357	( GGGGF	KGGGG	< KKGGG	( KKKGG	KKKKG	! Aao06186	₹ GG	< RGG	! Aao05665
	Human							Human					Human						Human			
	Human polypeptide							polypeptide					polypeptide						polypeptide			Human polypeptide SEQ
	SEQ							SEQ					SEQ						SEQ			
	ID NO							ID NO					ID NO						ID NO			ID NO
	20814.							20321					20249						20078			NO 19557
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(R,K){20}

KNPIK KKKKKKKKKKKKKKKKKKKKKK GGGF
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                                                                                                                                                                                                                                        AAO07410 ck: 693
                                                                                                                                                                                                                                                           (\kappa)\{20\}
39: HLKKK KKKKKKKKKKKKKKKKKKKKKK GGPLK
                                                                                                                                                                                                                                                                                (K){20}
                                                                                                                                                                                                                                                                                                    (K){20}
                                                                                                                                                                                                                                                                                                                        AA007354 ck: 6513 len: 133 ! Aa007354 Human polypeptide SEQ ID NO 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAO07241 ck: 3134 len: 40 ! Aao07241 Human polypeptide SEQ ID NO 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (K) {20}
                                                                                                                                                                                                                                        len: 80
                                                                                                                                                                                                                                     ! Aao07410 Human polypeptide SEQ ID NO 213
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20:	19:	18:	17:	AAC	23:	22:	21:	20:	19:	18:	17:	16:	15:	14:	AAC	107:	106:	105:	104:	103:	102:	101:	100:
XEKKK	KXEKK	VKXEK	KVKXE	AA007509	KKKKK	KKKKK	KKKKK	KKKKK		AKKKK		VEAKK	LVEAK	нглеч	AA007505	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX
(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K) {20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 4998 len: 140	(K)(20)	(K){20} KKKKKKKKKKKKKKKKKKKK	(K)(20)	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KXKKKKKKKKKKKKKKKKKK	(K){20} EAKKK KKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKK KKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 3528 len: 72	(K) {20} KKKKKKKKKKKKKKKKKKK	(K)[20] KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) {20} KKKKKKKKKKKKKKKKKKK	(K){20}	KKKKKKKKKKKKKKKKKKK KKKKK
KKKKK	KKKKK .	KKKKK	XXXXX	! Aao07509 Human polypeptide SEQ ID NO 21401.	DSRGG	KDSRG	KKDSR	KKKDS	KKKKD	KKKK	KKKKK	KKKKK	KKKKK	KKKKK	! Aao07505 Human polypeptide SEQ ID NO 21397.	GGENN	KGGEN	KRGGE	KKKGG	KKKKG	KKKKK	XXXX	KKKKK
	ı			<b>⊢</b>						1													

	19: TELTI	AA007610	48: GLFXE	21: kkke	AA007607	13: GKKKK	12: LGKKK	11: LLGKK	10: LLLGK	9: FLLLG	AA007594	32: KKKKK	31: KKKKK	30: KKKKK	29: KKKKK	28: KKKKK	27: KKKKK	26: KKKKK	25: KKKKK	24: KKKKK	23: KKKKK	22: KKKKK	21: EKKKK
(K){20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKK	ck: 5270 len: 74	(K) {20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKK	ck: 2434 len: 72	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKK	ck: 7271 len: 93	(K) [20] KKKKKKKKKKKKKKKKKKKK	(K){20}	(K) [20]									
	KKKKK	! Aao07610 Human polypeptide SEQ ID NO 21	GGGLF	GGGLF	! Aao07607 Human polypeptide SEQ ID NO 21	TKKNE	KTKKN	KKTKK	KKKTK	KKKKT	! Aao07594 Human polypeptide SEQ ID NO 21	GGGAS	KGGGA	KKGGG .	KKKGG	KKKKG	KKKKK						

46: РНХРЕ	AA007775	22: XKKKK	21: LXKKK	20: SLXKK	19: PSLXK	18: IPSLX	AA007762	42: KKKKK	41: KKKKK	40: KKKKK	39: SKKKK	38: SSKKK	37: QSSKK	36: NQSSK	35: KNQSS	AA007755	26: KKKKK	25: KKKKK	24: KKKKK	23: IKKKK	22: TIKKK	21: LTIKK	
(R, K) (20) (K) (20) E KKKKKKKKKKKKKKKKKKKK	ck: 9827 len: 90	(K) [20] KKKKKKKKKKKKKKKKKKKKKK	(K)(20)	(K){20}	(K){20}	(R,K){20} (K){20}	ck: 5115 len: 41	(K){20}	(R,K){20} (K){20}  KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 6069 len: 90	(K){20}	(K){20}	(K){20}	(K){20}	(K){20}	(K){20}							
KKKKK	! Aao07775 Human polypeptide SEQ ID NO 21667.		×	KK .	XXX	KKKK	! Aao07762 Human polypeptide SEQ ID NO 21654.	GGPLL	KGGPL	KKGGP	KKKGG	KKKKG	KKKKK	KKKKK	KKKKK	! Aao07755 Human polypeptide SEQ ID NO 21647.	GGGAL	KGGGA	KKGGG	KKKGG .	KKKKG ·	KKKKK	NAME OF THE PARTY

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(R,K){20}
(K){20}
52: TKKKQ KKKKKKKKKKKKKKKKKKKKK GGGLL
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(K){20}
                                               (K)(20)
91: EPSIK KKKKKKKKKKKKKKKKKKKK G
                                                                                                                                                                AAO07874 ck: 8007 len: 111 ! Aao07874 Human polypeptide SEQ ID NO 217
                                                                                                                                                                                                                         AAO07872 ck: 8003 len: 135 ! Aao07872 Human polypeptide SEQ ID NO 217
                                                                                                                                                                                                                                                  (K){20}
                                                                                                                                                                                                                                                                         (K){20}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAO07806 ck: 1959 len: 99
                       (K){20}
                                                                                 AAO07876 ck: 8130 len: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ! Aao07806 Human polypeptide SEQ ID NO 216
                                                                               | Aao07876 Human polypeptide SEQ ID NO 217
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(K){20}	57: IYKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20) 56: CIYKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20) (K)(20)	(R,K)[20] (K)[20] 54: KPCIY KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAO07981 ck: 9551 len: 81 ! Aao07981 Human polypeptide SEQ ID NO 2	55: KKKKK KKKKKKKKKKKKKKKKK ASSGG	(K){20} 54: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	53: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	52: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20] 51: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20)  50: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20)	48: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	47: TKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	46: STKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20] 45: ISTKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 44: PISTK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} 43: FPIST KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAOO7976 ck: 6471 len: 97 ! Aao07976 Human polypeptide SEQ ID NO	23: KKKKK KKKKKKKKKKKKKKKKKKKKK QKKEN	22: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) [20] 21: EKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 20: FEKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
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AAO08458 ck: 1813 len: 59
                                                                                                                                                                                                        AAO08450 ck: 6228 len: 31
                                                                                                                                                                            (K)(20)
50: SQQNK KKKKKKKKKKKKKKKKKKKKKK DGGGA
                                                                                                                                                                                                                                         AA008232 ck: 782 len: 104 ! Aao08232 Human polypeptide SEQ ID NO 22
                                                                                                                                                                                                                                                                                                      AAO08121 ck: 5381 len: 86 | Aao08121 Human polypeptide SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                  AAO08018 ck: 9768 len: 48 ! Aao08018 Human polypeptide SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (K){20}
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7: NSAKK KKKKKKKKKKKKKKKKKKKKKK GGAAF
                                                                                      (K){20}
                                                                                                                (R,K){20}
(K){20}
NNSA KKKKKKKKKKKKKKKKKKKK KKGGA
                                ! Aao08458 Human polypeptide SEQ ID NO 22
                                                                                                                                                 ! Aao08450 Human polypeptide SEQ ID NO 22
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60:	<b>1</b>	59:	5 <b>8</b> :	57:	AAO	3 <b>4</b> :	33:	32:	31:	30:	29:	28:	27 :	26:	25:	24:	23:	22:	AAC	13:	12:	11:	10:	9:
GVKKK		GGVKK	WGGVK	FWGGV	AAO08466	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	TKKKK	STKKK	FSTKK	EFSTK	KEFST	AAO08460	KKKKK	EKKKK	WEKKK	GWEKK	GGWEK
		(K) (20)	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKK	ck: 8728 len: 107	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) (20)	(K){20}	(K){20}	(K) {20}	(K) (20)	(K){20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKK	ck: 5334 len: 62	(K)(20)	(K){20}	(K){20}	(K){20}	(K){20}
KKRRK		KKKRR	KKKKR	KKKKK	! Aao08466 Human polypeptide SEQ ID NO 22358.	1KKKG	KIKKK	KKIKK	XXXIX	KKKKI	KKKKK	KKKKK	XXXXX	KKKKK	XXXXX	XXXX	KKKKK	KKKK	! Aao08460 Human polypeptide SEQ ID NO 22352.	NKKKK	KNKKK	KKNKK	KKKNK	KKKKN
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	9:	œ ::	7:	6:	i	23:	22:	21:	20:		AAO	19:	18:	AAO	14:	AAO	, u	} }		65 6 5 4		0 0	) <u> </u>	<u>5</u>

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(K){20}
                                                                (K){20}
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(K)(X)
                                                                                                                                                                                                       (R,K)[20]
(K)[20]
KKKKKKKKKKKKKKKKKKKKKK GGAFK
                                                                                                                                      008616 ck: 4555 len: 41 ! Aao08616 Human polypeptide SEQ ID NO 225
                                                                                                                                                                                                                                                                                                             008612 ck: 557 len: 46 ! Aao08612 Human polypeptide SEQ ID NO 225
                                                                                                                                                                                                                                                                                                                                                (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                       008591 ck: 900 len: 46 ! Aao08591 Human polypeptide SEQ ID NO 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (R,K)[20]
(K)[20]
EPILL KKKKKKKKKKKKKKKKKKKKK GGALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .008580 ck: 5164 len: 62 | Aao08580 Human polypeptide SEQ ID NO 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (R,K){20}
: KKKKK KKKKKKKKKKKKKKKKKKR RKGRK
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(K){20}
LPKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (R,K)(20)
KKKKK KKKKKKKKKKKKKKKKKRR KGRKE
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(K)[20]

10: PKKKK KKKKKKKKKKKKKKKKKKK KKKKK

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AAO08631 ck: 6430 len: 135 ! Aao08631 Human polypeptide SEQ ID NO 22523
                                                                                                                                                                                    (R,K){20}

(K){20}
                                                                                                                                                                                                                                             (R,K)[20]
(R,K)[20]
21: DSKQE KKKKKKKKKKKKKKKKKKKKKKKKKGGAFK
                                                          16: KKKKK KKKKKKKKKKKKKKKKKK WGGAL
                                                                                  (K){20}
15: WKKKK KKKKKKKKKKKKKKKKKKKK KWGGA
                                                                                                          AAO08623 ck: 9243 len: 119 ! Aao08623 Human polypeptide SEQ ID NO 22515
                                                                                                                                                                                                                                                                                                      21: KKKKK KKKKKKKKKKKKKKKKKK K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAO08624 ck: 5590 len: 65
                                                                                                                                                                                                                  ! Aao08624 Human polypeptide SEQ ID NO 22516.
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10:	9:	8	7:	6.	<u>ن</u>	<b>.</b>	ω 	2:	AAC	44:	43:	42:	41:	40:	39:	38:	37:	36:	35 :	3 4	33:	32:	31:
KKKKK	KKKKK	KKKKK	KKKKK	EKKKK	EKKK	EKK	EK	tri	AAO08644	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	AKKKK	RAKKK	SRAKK	PSRAK
(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 3202 len: 80	(R,K){20} KKKKKKKKKKKKKKKKKKR	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K) (20) KKKKKKKKKKKKKKKKKKK	(K){20}	(K) {20} KKKKKKKKKKKKKKKKKKKK	(K){20}
KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	! Aao08644 Human polypeptide SEQ ID NO 22!	GGGPK	RGGGP	KRGGG	KKRGG	KKKRG	KKKKR	KKKKK	KKKKK	KKKKK	KKKKK .	KKKKK	KKKKK	KKKKK	KKKKK

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	25:	24:	23:	00	20:	9:	18:	17:	16:	15:	14:	13:	12:	A00	9.		7:	6:	15:		13:	2 :	11:
	VNHKK	PVNHK	нилан	AAO08686	KKKKK	KKKKK	KKKKK	KKKKK	TKKKK	LTKKK	KLTKK	IKLTK	PIKLT	AAO08653	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
(K) (20)	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 6936 len: 81	(R,K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(#){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKK	ck: 6448 len: 63	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20} KKKKK KKKKKKKKKKKKKKKKKK KKKKG	(K) {20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK
_	KKKKK	KKKKK	KKKKK	! Aao08686 Human polypeptide SEQ ID NO 22578.	GAPLK	RGAPL	KRGAP	KKRGA	KKKRG	KKKKR	KKKKK	KKKKK	KKKKK	! Aao08653 Human polypeptide SEQ ID NO 22545.	GGGGP	KGGGG	KKGGG	KKKGG	KKKKG	KKKKK	KKKKK	XXXXX	KKKKK
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AAO	13:	12:	11:	10:	9:	œ 	7:	AAO	37:	36:	35:	34:	33:	32:	31:	30:	29:	28:	27 :	26:
AA008707	KKKKK	KKKKK	SKKKK	NSKKK	ANSKK	NANSK	INANS	AA008701	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	HKKKK	NHKKK
 ck: 9359 len: 48	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 588 len: 46	(K){20} KKKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	KKKKKKKKKKKKKKKKKKK
! Aac08707 Human	GGGTT	KGGGL	KKGGG	KKKGG	KKKKG	KKKKK	KKKKK	! Aao08701 Human	EGALG	KEGAL	KKEGA	KKKEG	KKKKE	KKKKK	KKKKK	KKKKK	KKKKK	C KKKKK	C KKKKK	C KKKKK
n polypeptide								n polypeptide												
SEQ ID N				•				SEQ ID N												
NO 225								NO 225												

(K){20}
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19: KLKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	18: IKLKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	17: TIKLK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R.K)(20)  (R)(20)  (K)(20)  (K)(20)	(K){20} K KKKKKKKKKKKKKKKKK GGGPF	29: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	28: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20}	YLKKK	(K) (20) 25: NYLKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	24: MNYLK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20}  23: IMNYL KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAO08772 ck: 1431 len: 105   Aao08772 Human polypeptide SEQ ID NO 22664.	80: SELLI KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAO08717 ck: 4688 len: 99 ! Aao08717 Human polypeptide SEQ ID NO 22609.	13: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	12: PKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	11: FPXKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	10: TFPKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	9: MTFPK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)(20) (K)(20)  8: SWTFP KKKKKKKKKKKKKKKKK KKKKK	AAO08708 ck: 9654 len: 32 ! Aao08708 Human polypeptide SEO ID NO 22600.
(K){20}	10: IKSFK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	1 (R,K){20} (K){20} 9: IIKSF KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 30: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK		28: TSKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK		25: PPPTS KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)(20)	AAO08857 ck: 2816 len: 49 ! Aao08857 Human polypeptide SEO ID NO 22	4: POK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	1 (R,K){20} (K){20} 3: PQ KKKKKKKKKKKKKKKKKK KWGGG	AAOO8841 ck: 3529 len: 74   AaoO8841 Human polypeptide SEQ ID NO 22	29: MTFSK KKKKKKKKKKKKKKKKKKKK GGGFI	1 (R,K)(20) (K)(20) 28: CMTFS KKKKKKKKKKKKKKKKK RGGGF	. AAOO8820 ck: 1888 len: 84 ! AaoO8820 Human polypeptide SEQ ID NO 22	3: AX KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAO08817	23: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	22: KKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) [20] 21: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	20: LKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK

	AAOC	6.	AAOC	31:	30:	29:	28:	27 :	26:	25:	24:	23:	22:	21:	20:	19:	18:	17:	16:	15:	14:	13:	12:
	AAO08943	ILMPX	AAO08914	KKKKK	KKKKK	XXXXX	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	XXXXX	FKKKK	SFKKK
(K) {20}	ck: 5770 len: 75 ! Aao08943 Human polypeptide SEQ ID NO 22835 (R,K) (20)	K) {20}	ck: 4641 len: 25 ! Aao08914 Human polypeptide SEQ ID NO 22806	(K){20} KKKKKKKKKKKKKKKKK II	(K)(20)	(K)(20)	(K)(20)	KKKKKKKKKKKKKKKKK KKKKI	(K)[20]	KKKKKKKKKKKKKKKKK KKKKK	KKKKKKKKKKKKKKKKK KKKKK	(K)(20)	(K)[20]	KKKKKKKKKKKKKKKKK KKKKK	(K)(20) KKKKKKKKKKKKKKKKK KKKKK	(K)[20] KKKKKKKKKKKKKKKKK KKKKK	(K)[20]	(K)[20] KKKKKKKKKKKKKKKKK KKKKK	KKNKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20)	KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20]	KKKKKKKKKKKKKKKKK KKKKK
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10: KKKKK KKKKKKKKKKKKKKKKKKK GGGPF
                                                                                                                                                                                                                  AAO09057 ck: 3712 len: 58
                                                                                                                                                                                                                                                  (R,K){20}
(R,K){20}
10: EEEEE RRKKRRRRRKKRKKKK ILROK
                                                                                                                                                                                                                                                                                            AAO09016 ck: 4378 len: 119 | Aao09016 Human polypeptide SEQ ID NO 229
                                                                                                                                                                                                                                                                                                                                                                                                                                           AA009001 ck: 6400 len: 26 ! Aao09001 Human polypeptide SEQ ID NO 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAO08995 ck: 6270 len: 26 ! Aao08995 Human polypeptide SEQ ID NO 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAO08994 ck: 2695 len: 29
                                                                                                                                                                    (R,K)[20]
(K)[20]
6: MAAPP KKKKKKKKKKKKKKKKKKKK I
                                                                6: MILNK KKKKKKKKKKKKKKKKKKKKKKKKKKKK
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                                (K)(20)
ILNKK KKKKKKKKKKKKKKKKKKKKKKKKKKGG
                                                                                                                                                                                                             ! Aao09057 Human polypeptide SEQ ID NO 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ! Aao08994 Human polypeptide SEQ ID NO 228
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AAO09066 ck: 2645 len: 29

! Aao09066 Human polypeptide SEQ ID NO 229

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(K){20}
                                                                   AAO09162 ck: 3841 len: 100 ! Aao09162 Human polypeptide SEQ ID NO 23054
                                                                                                                                             (K){20}
                                                                                                                                                                                         (K)(20)
27: FLLTK KKKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                       AAO09072 ck: 8432 len: 42
                                              12: TLFQK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                       30: TKKKK KKKKKKKKKKKKKKKKKKK WGGGG
                                                                                                                                                                                                                                               AAO09077 ck: 9524 len: 87
                                                                                                                                                                                                                                                                     (K){20}
                                                                                                                                                                                                                                                                                           13: TTLKK KKKKKKKKKKKKKKKKKKKK KEKYE
                                                                                                                                                                                                                                                                                                                 (K){20}
                                                                                                                                                                                                                                                                                                                                                                                            (K){20}
9: KKKKK KKKKKKKKKKKKKKKKKK K
                                                                                                                                                                                                                                                                                                                                                                                                                                        5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ! Aao09072 Human polypeptide SEQ ID NO 22964
                                                                                                                                                                                                                                            ! Aao09077 Human polypeptide SEQ ID NO 22969
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ມ ວ	AAO	12:	11:	10:	9:	æ 	7:	AAO	29:	28:	27:	26:	25:	24:	23:	22:	21:	20:	19:	18:	17:	16:	15:
NTCMT	AA009269	KKKKK	PKKKK	CPKKK	FCPKK	LFCPK	LLFCP	AA009258	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	OKKKK								
(R, K) (20) (R, K) (20)	ck: 7553 len: 106   Aao09269 Human polypeptide SEQ ID NO 23	(K)(20) KKKKKKKKKKKKKKKKKK GGPIK	(K)[20] KKKKKKKKKKKKKKKKKKK KGGPI	(K)[20] KKKKKKKKKKKKKKKKKKK KKGGP	(K)[20]	(K)[20]	(R,K)[20] (K)[20] KKKKKKKKKKKKKKKKKK KKKKK	ck: 7988 len: 42 ! Aao09258 Human polypeptide SEQ ID NO 23	(R,K){20}	(K)[20] KKKKKKKKKKKKKKKKKK RGGGA	(K)[20] KKKKKKKKKKKKKKKKKK KRGGG	(K)[20] KKKKKKKKKKKKKKKKKKK KKRGG	(K)[20] KKKKKKKKKKKKKKKKKK KKKRG	(K)[20]	(K)(20)	(K)[20]	(K)[20]	(K)[20]	(K)(20)	(K)[20]	(K)[20]	(K)[20]	(K)[20] KKKKKKKKKKKKKKKKKK KKKKK

39: NTGML KKKKKKKKKKKKKKKKKKKK GGPFL

(R,K){20} (K){20} 42: CRLSE KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAO10608 ck: 9106 len: 67 ! Aao10608 Human polypeptide SEQ ID NO 24500.	20: LTLKK KKKKKKKKKKKKKKKKKK EMPVK	(K)[20] 19: LLTLK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} 18: NLLTL KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAO10564 ck: 9156 len: 98   Aao10564 Human polypeptide SEQ ID NO 24456.	58: CEFMK KKKKKKKKKKKKKKKKKK IGGGA	57: KCEFM KKKKKKKKKKKKKKKKK KIGGG	AAO10467 ck: 7542 len: 116 ! Aao10467 Human polypeptide SEQ ID NO 24359. (R,K)(20)	P KKKKKKKKKKKKKKKK AR	(R,K){20} (K){20}	AAO10451 ck: 3955 len: 82 ! Aao10451 Human polypeptide SEQ ID NO 24343.	30: KKKKK KKKKKKKKKKKKKKKKK I	29: LKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	28: KLKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	27: LKLKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	26: FLKLK KKKKKKKKKKKKKKKKK KKKKI	25: RFLKL KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)(20)	AAO10447 ck: 6342 len: 50 ! Aao10447 Human polypeptide SEO TD NO 24339	(K)(20) 54: CFFVX KKKKKKKKKKKKKKKKK EKGGG	(R,K){20}	09819	(R,K)(20) (K)(20) 9: ALVPQ KKKKKKKKKKKKKKKKK NIKI	AAO09457 ck: 9658 len: 32 ! Aao09457 Human polypeptide SEQ ID NO 23349.
(K)[20] 21: SRXMK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	1 (R,K){20} (K){20} 20: FSRXM KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAO10852 ck: 5147 len: 41   Aao10852 Human polypeptide SEQ ID NO 247	(K)(20) 35: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20) 34: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	33: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	32: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	31: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	30: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	29: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 28: SKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	27: FSKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	26: XESKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	25: PXFSK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) {20} 24: CPXFS KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAO10786 ck: 7349 len: 65 ! Aao10786 Human polypeptide SEQ ID NO 246	* ************************************		33: CEPOP KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAO10638 ck: 621 len: 56 ! Aao10638 Human polypeptide SEQ ID NO 245		46: EKKKK KKKKKKKKKKKKKKKKKKK JA	45: SEKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 44: LSEKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	43: RLSEK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK

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(K){20}
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28: KKKKK KKKKKKKKKKKKKKKKKKK RGELX
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                                                                                                                        AAO10859
                                                                                                                                             29: KKKKK KKKKKKKKKKKKKKKKKK GELXK
                                                                                                                                                                                                                  26: KKKKK KKKKKKKKKKKKKKKKKKK KKRGE
                                                                                                                                                                                                                                                                                                            22: KKKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                          20: KKKKK KKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAO10853 ck: 444 len: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (K){20}
22: RXMKK KKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ck: 2690 len: 70
(K)[20]
                                            len:
                                             69
                                        ! Aao10933 Human polypeptide SEQ ID NO 24825
                                                                                                                    ! Aao10859 Human polypeptide SEQ ID NO 24751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! Aao10853 Human polypeptide SEQ ID NO 24745
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AAO10995 ck: 2382 len: 122
                                                   29: KKKKK KKKKKKKKKKKKKKKKKKKK TGG
                                                                       (K)[20]
28: XKKKK KKKKKKKKKKKKKKKKKKK KTGG
                                                                                            (K){20}
                                                                                                                  26: ILXKK KKKKKKKKKKKKKKKKKKK KKKTG
                                                                                                                                       (K){20}
                                                                                                                                                            AAO10983 ck: 694
                                                                                                                                                                                                               (K){20}
                                                                                                                                                                                                                                                                   AAO10973 ck: 824
                                                                                                                                                                                                                                                                                        (K){20}
                                                                                                                                                                                                                                                                                                            (K){20}
                                                                                                                                                                                                                                                                                                                                                       41: KKKKK KKKKKKKKKKKKKKKKK KKKKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36: TEKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (R,K)(20)
                                                                                                                                                                                          len: 51
                                                                                                                                                                                                                                                                   len: 51
                           ! Aao10995 Human polypeptide SEQ ID NO 24
                                                                                                                                                                                                                                                                ! Aao10973 Human polypeptide SEQ ID NO
                                                                                                                                                                                        ! Aao10983 Human polypeptide SEQ ID NO 24
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54: I	53: 1	AAO11	11: 3	10: (	AAO11033	38:	<del>ن</del> :-	AA011002	35:	3 <b>4</b> ::	33 :	32 :	31:	30:	29:	AA010997	28:	27:	26:	25:	24:	23:
SDPK	ISDP	1048	XKFIR	OXKFI	1033	XFKRS	FKRS	1002	KKKKK	KKKKK	QKKKK	IQKKK	1 IQKK	XIIQK	OLİXI	0997	KKKKK	KKKKK	SKKKK	GSKKK	KGSKK	CKGSK
(K) {20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKK	ck: 7868 len: 85	(K){20} KKKKKKKKKKKKKKKKKKKK	(R, K) (20) (R, K) (20) RKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 3780 len: 49	(R,K)(20) KKKKKKKKKKKKKKKKKKR	(R,K){20} (R,K){20} KKKKKKKKKKKKKKKKKKKK	ck: 8638 len: 82	(R,K){20} KKKKKKKKKKKKKKKKKKKK	(K) {20} KKKKKKKKKKKKKKKKKKK	(K)(20) OKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) (20) KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 5315 len: 58	(K) [20] KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K)(20)	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK KKKKK
KKKKK	KKKKK	! Aaoll048 Human	LSKKI	KLSKK	1 Aaol1033 Human	GGALL	GGALL	! Aao11002 Human	GGPP	RGGPP	KRGGP	KKRGG	KKKRG	KKKKR	XXXXX	! Aao10997 Human polypeptide	GGGGF	KGGGG	KKGGG	KKKGG	KKKKG	KKKKK
		Human polypeptide SEQ			polypeptide SEQ			polypeptide SEQ								polypeptide SEQ						
		ID NO 24940.			) ID NO 24925.			) ID NO 24894.				_				Q ID NO 24889.						
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<b>4</b> 8:	47:	46:	45:	44:	43:	42:	41:	40:	39:	AAO:	66:	65:	64:	63:	62:	61:	60:	59:	58:	57:	56:	55:
KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	DKKKK	PDKKK	KPDKK	PKPDK	PPKPD	11078	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	PKKKK	DPKKK	SDPKK
	(K)(20) K KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20] K KKKKKKKKKKKKKKKKKKK KKKKK	K KKKKKKKKKKKKKKKKK KKKKK	K KKKKKKKKKKKKKKKKK KKKKK	(K)(20)	K KKKKKKKKKKKKKKKKKK KKKKK	(K){20}	K KKKKKKKKKKKKKKKKK KKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKK KKKKK	ck: 4186 len: 100 ! Aao11078	(K)(20) K KKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20}	(K){20}	(K){20}	(K){20}	(K)(20) (K)(20)	(K.)(20)	(K)(20)  KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K.){20}	(K)(20)
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	(K)(20)  KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20) 7: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20]  (K)[20]  (K)[20]  (K)[20]  (K)[20]  (K)[20]  (K)[20]  (K)[20]	(K)[20]   (K) [20]   (K) [20]  : KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) [20]  : DKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) [20]   (K) [20]   (R, K) [20]  (K) [20]	(R,K)[20] (R,K)[20] (R)[20]	(K)(20) (R,K)(20) (R,K)(20) (R,K)(20) (R)(20)	(K)[20] (K)[20] (R)[20] (R)[20] (R, X)[20] (R, X)[20] (R, X)[20] (R, X)[20] (R)[20] (R	(K)[20]  KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20]  (K)(20]   (K)[20]  KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20]  KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20]  KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20)  KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	S: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)[20]  KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) [20]  RKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK					

35: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	34: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	33: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	32: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	31: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	30: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	29: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	28: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	27: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	26: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	25: KKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK		24: KXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	23: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	22: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	21: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	20: LKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) (20) 19: FLKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	18: SFLKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) (20) 17: YSFLK KKKKKKKKKKKKKKKKKK KKKKK	(R,K)(20) (K)(20)	AAO11124 ck: 5121 len: 61 ! AaO11124 Human polypeptide SEQ ID NO 25016.	52: KKKKK KKKKKKKKKKKKKKKKK GGGGF	(K)(20) 51: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	50: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	_
(K){20} 64: ELÞYK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	63: LLLAY KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAO11209 ck: 6562 len: 96 ! Aao11209 Human polypeptide SEQ ID NO 25:	26: KKKKK KKKKKKKKKKKKKKKKKKKK ASSSQ	25: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	KKKKK	7		(K)[20]  (K)[20]  (K)[20]	. (K)[20] 21: MVKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	20: SMVKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	19: ASMYK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	18: DASMV KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	1 (R,K)(20) (K)(20)	-AAO11165 ck: 7203 len: 62 ! Aao11165 Human polypeptide SEQ ID NO 25	(K){20} (K){10}	(R,K){20} (K){20} 22: VCRFP KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAO11139 ck: 8807 len: 68 ! AaO11139 Human polypeptide SEQ ID NO 25	(K){20} 42: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K) (20) 41: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} 40: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	39: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	38: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	37: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	36: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	

24: KKKKK	23: XKKKK	22: CXKKK	21: VCXKK	20: RVCXK	19: NRVCX	AA011214	45: KKKKK	44: KKKKK	43: KKKKK	42: KKKKK	41: KKKKK	40: KKKKK	39: KKKKK	38: KKKKK	37: KKKKK	36: KKKKK	35: CKKKK	34: LCKKK	33: CLCKK	32: LCLCK	31: DLCLC	AA011210	65: LAYKK
(K)(20)	(K)(20)	(K){20}	(K){20} "	(K)(20)	(R,K)[20] (K)[20] KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 9584 len: 68	( KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20}	(K){20}	(K){20}	(K) (20)	(K){20}	(K){20}	(K){20}	(K)[20]	(K){20}	(K){20}	(K){20}	(R, K) [20] (K) [20] KKKKKKKKKKKKKKKKKKKKKKK	ck: 863 len: 70	(K){20}
RGGPL	KRGGP	KKRGG	KKKRG	KKKKR	KKKKK	! Aao11214 Human polypeptide SEQ ID NO 25106.	POGGG	KPQGG	KKPQG	KKKPO	KKKKP	ベスススス	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KRKKK	KKKKK	KKKKK	Aao11210 Human polypeptide SEQ ID NO 25102.	PKYLS
		-	a.															٢			1		

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AA011324 ck: 6024 len: 93 / Aa011324 Human polypeptide SEQ ID NO 252
                                                                                                                                      (K){20}
                                                                                                                                                                                                                           AA011293 ck: 6490 len: 73 ! Aa011293 Human polypeptide SEQ ID NO 251
                                                                                                                                                                                                                                                     (K){20}
                                                                                                                                                                                                                                                                                                      (K)(20)
55: XKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK
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                                                                                                                                                                (K){20}
                                                                                                                                                                                                                                                                              (K){20}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAO11241 ck: 1100 len: 36 ! AaO11241 Human polypeptide SEQ ID NO 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25: KKKKK KKKKKKKKKKKKKKKKKK GGPLK
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	••	7: NPPVS	AAO:11799	20: LQKKK	19: РЬДКК	18: APLQK	17: WAPLQ	AAO11705	26: IFKXK	25: SIFKX	AAO11352	62: ANHWE	AA011346	61: FFKTX	AAO11342	23: ELKKK	22: KELKK	21: SKELK	20: LSKEL	AA011327	40: SARKK
		(R,K){20} (R,K){20}	ck: 8286 len: 39	(K){20}	(K){20}	(K){20}	(R, K) {20} (K) {20}	ck: 7660 len: 101	(K) (20)	(R,K)[20] (K)[20]  KKKKKKKKKKKKKKKKKKKKKKK	ck: 1342 len: 51	(R,K)[20] (K)[20] KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 7311 len: 85	(R,K){20} (K){20}	ck: 7189 len: 106	(K){20}	(K) [20]	(K){20}	(R,K)[20] (K)[20]	ck: 3052 len: 102	(K) (20)
RAKKK		KKKKK	! Aao11799 Human polypeptide SEQ ID NO 25691.	GGAPL	KGGAP	KKGGA	KKKGG	! Aaol1705 Human polypeptide SEQ ID NO 25597.	NPPSL	KNPPS	! Aaol1352 Human polypeptide SEQ ID NO 25244.	saca	! Aaol1346 Human polypeptide SEQ ID NO 25238.	GGPLK	! Aaoll342 Human polypeptide SEQ ID NO 25234.	LGDEE	KLGDE	KKLGD	KKKLG	! Aao11327 Human polypeptide SEQ ID NO 25219.	GGGCV

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AA011831 ck: 1761 len: 29
                                                                                                                                                                                                                                                              AAO11820 ck: 8725 len: 42
                                                                                                                                                                                                                                                                                                                                      (K){20}
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                                                                                                                                                                                                                                                                                                      (K){20}
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                                              <u>..</u>
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                                                                                    (R,K){20}
9: KKKKK KKKKKKKKKKKKKKKKKKK GGGFK
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KKKK KKKKKKKKKKKKKKKKKK KKKRG
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           (R,K){20}
(K){20}
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                                                                                                                                                                                                                                                                                    ! Aao11820 Human polypeptide SEQ ID NO 25
                                                                                                                                                                                                                                              ! Aao11828 Human polypeptide SEQ ID NO 25
                                                                 ! Aaol1831 Human polypeptide SEQ ID NO 25
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13:
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                                                                                                      AAO11844 ck: 3574 len: 49
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د
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                                                                                                                                           (K){20}
                  MEKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK
                                     LYMEK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                            (K) (20)
KKKKK KKKKKKKKKKKKKKKK SG
                                                                                                                                                                KKKKK KKKKKKKKKKKKKKKKK KKKSG
                                                                                                                                                                                                       (K){20}
                                                                                                                                                                                                                                             (K)(20)
                                                                                                                                                                                                                                                                 (K){20}
                                                                                                                                                                                                                                                                                    (K){20}
                                                                                                                                                                                                                                                                                                       (K){20}
KKKK KKKKKKKKKKKKKKKKKK AGGGA
                                                                                                                                                                                                                                                                                                                         (K){20}
                                                                                                                                                                                                                                                                                                                                              (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                       (K) (20)
                                                                                                                                                                                                                                                                                                                                                                                                                                  len: 36
                                                                                                    ! Aao11844 Human polypeptide SEQ ID NO 25736
                                                                                                                                                                                                                                                                                                                                                                                                                                  ! Aao11843 Human polypeptide SEQ ID NO 25735
```

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AAO11886 ck: 5282
                             (R,K)(20)
17: EKKKK KKKKKKKKKKKKKKKKKRKR
                                                                                 15: LCEKK KKKKKKKKKKKKKKKKKKK KR
                                                                                                                                   (R,K){20}
                                                                                                          (K){20}
                                                                                                                                                                                                                           (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAO11849 ck: 284
                                                                                                                                                                                                  24: KKKKK KKKKKKKKKKKKKKKKKK TG
                                                                                                                                                                                                                                                                                                        19: LKKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                           (K){20}
                                                                                                                                                                                                                                                                                                                                                                                     27: KKKKK KKKKKKKKKKKKKKKKK YSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16: PSTLK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAO11845 ck: 8375 len: 45
                                                                                                                                                                                                                                                                               (K){20}
KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKTG
   len: 97
                                                                                                                                                                        len: 36
! Aaol1886 Human polypeptide SEQ ID NO 257
                                                                                                                                                                       ! Aaol1849 Human polypeptide SEQ ID NO 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ! Aao11845 Human polypeptide SEQ ID NO 257
```

3 3 3 3 3 3 3 3 3 3 3 3 5 3 3 5 3 5 5 5 5 5 6 5 6
NSSLK SSLKK SLKKK LKKKK KKKKK
(K)[20]  KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
(%)(10)

```
(K){20}
                       (K){20}
                                  AAO12098 ck: 8434 len: 39 ! Aao12098 Human polypeptide SEQ ID NO 25
                                                                         (K){20}
                                                                                    20: GLKKK KKKKKKKKKKKKKKKKKKKKKKKKKKG
                                                                                                                                   AAO11999 ck: 3954 len: 47 ! Aao11999 Human polypeptide SEQ ID NO 25
                                                                                                                                                                                                 (K){20}
                                                                                                                                                                                                                                               (K){20}
```

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AA012180
                                      46:
                                                           (K){20}
                                                                                  (K){20}
                                                                                                            43:
                                                                                                                                  42:
                                                                                                                                                          41:
                                                                                                                                                                              (R,K)(20)
(K)(20)
(K)(20)
                                                                                                                                                                                                                                                                                                                                                     58: KKKKK KKKKKKKKKKKKKKKKK ARG
                                                                                                                                                                                                                                                                                                                                                                           (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                   56:
                                                                                                                                                                                                                                                                                                                                                                                                                        (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                               54: ATSEK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAO12179 ck: 1295 len: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAO12105 ck: 6255 len: 80
                                    (K){20}
KKKKK KKKKKKKKKKKKKKKKKK GGGA
                                                                                                          (K)(20)
KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKGG
                                                                                                                                (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                  ck: 9840 len: 67
(R,K)(20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (R,K)[20]
          ! Aao12180 Human polypeptide SEQ ID NO 26072
                                                                                                                                                                                                                                                                                                                            ! Aao12179 Human polypeptide SEQ ID NO 26071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ! Aao12105 Human polypeptide SEQ ID NO 25997
```

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(K){20}
                                                                   (K){20}
                                                                             (K){20}
                                                                                       (K){20}
                                                                                                (K){20}
                                                                                                                                                            (x){20}
                                                                                                                                                                               (K){20}
                                                                                                             AAO12187 ck: 4700 len: 60
                                                                                                                                                                                                   (K){20}
                                                                                                                                                                                                                     38: CSYLP KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                            ! Aao12187 Human polypeptide SEQ ID NO 260
```

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(K){20}
                                  36: KKKKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                    35: LKKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                     (K){20}
                                                                                                                                                                                                        (R,K){20}
(K){20}
                                                                                                                                       33: SNEKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                         32: PSNLK KKKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                                                                                                                                                                             (R){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51: PFLPK KKKKKKKKKKKKKKKKKKKK TGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (R,K){20}
(K){20}
(K){20}
                                                                                                                                                                                                                                                       AAO12250 ck: 1538 len: 69
                                                                                                                                                                                                                                                                                       (K){20}
                                                                                                                                                                                                                                                                                                                                                            (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                             AAO12215 ck: 6903 len: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAO12203 ck: 4083 len: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAO12243 ck: 8474 len: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9: CLKKK KKKKKKKKKKKKKKKKKKKK PGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6: SWCCL KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ! Aao12243 Human polypeptide SEQ ID NO 26135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ! Aao12203 Human polypeptide SEQ ID NO 26095
                                                                                                                                                                                                                                                    ! Aao12250 Human polypeptide SEQ ID NO 26142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ! Aao12215 Human polypeptide SEQ ID NO 26107
```

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34: KKKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                        32: PLKKK KKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                               31: PPLKK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                            (K)[20]
17: INKKK KKKKKKKKKKKKKKKKK G
                                                                                                                                                                                                                                                                                                                                     (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30: IPPLK KKKKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                               (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40: KKKKK KKKKKKKKKKKKKKKKKKK KKKKR
                                                                                                                                                                                                                                           AAO12280 ck: 7481 len: 66
                                                                                                                                                                                                                                                                                         AAO12274 ck: 2739 len: 37
                                                                                                                                                                                                                                                                                                                                                                                            45: KKKKK KKKKKKKKKKKKKKKKKK GGGAF
                      (K){20}
                                           (K){20}
                                                                                                                                                                                                                                          ! Aao12280 Human polypeptide SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                     ! Aao12274 Human polypeptide SEQ ID NO 26
```

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(K){20}
                                                                                                                              (K){20}
10: CCFIK KKKKKKKKKKKKKKKKKKKKK RGAP
                                                                                                                                                                                                                                                                                         (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40:
                                                                     AAO13164 ck: 2798 len: 71
                                                                                                                                                                                                                                                                                                                                                               66: FCHQK KKKKKKKKKKKKKKKKKKK GFFFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39: KKKKK KKKKKKKKKKKKKKKKKK KKKSG
                                                                                                                                                                                                    AAO12553 ck: 1903 len: 33
                                                                                                                                                                                                                                (K){20}
                                                                                                                                                                                                                                                              39:
                                                                                                                                                                                                                                                                                                                                  AAO12548 ck: 6973 len: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                  AA012476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAO12447
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (R,K){20}
VCEKK KKKKKKKKKKKKKKKKKK GGALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (R,K){20}
CFIKK KKKKKKKKKKKKKKKKKKK GAP
                                                                                                                                                           VLPLK KKKKKKKKKKKKKKKKKKKK KGGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPPLX
                                                                                                                                                                                                                                                                                                                                                                                                                                   ck: 837
                            ck: 5017 len: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                   len: 104
                                                                                                                                                                                                                                                                                                                                                                                                                               ! Aao12476 Human polypeptide SEQ ID NO 26368
                                                               ! Aao13164 Human polypeptide SEQ ID NO 27056
                                                                                                                                                                                              ! Aao12553 Human polypeptide SEQ ID NO 26445
                                                                                                                                                                                                                                                                                                                              ! Aao12548 Human polypeptide SEQ ID NO 26440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ! Aao12447 Human polypeptide SEQ ID NO 26339
```

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(K){20}
                53: KKKKK KKKKKKKKKKKKKKKKKKKKKA,
                                57 :
                                                                                                                                                                                                                                                                                                                                  56:
                                                                                                                                                                                                                                                                                                                                                                                   (K){20}
                                                                                                    (K){20}
                                                                                                                                                      (K){20}
                                                                                                                                                                      (K){20}
                                                                                                                                                                                      (K){20}
                                                                                                                                                                                                                                                               60: KKKKK KKKKKKKKKKKKKKKKKK GGGPF
                                                                                                                                                                                                                                                                               (K){20}
                                                                                                                                                                                                                                                                                                                                                                  (K){20}
                                                                                                                                                                                                                                               AAO13785 ck: 6241 len: 100
                                                                                                                                                                                                                                                                                                                                                                                                         AAO13576 ck: 4846 len: 99
                                                                                                                                                                                                                                                                                                                 (K){20}
IKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                 (K){20}
                                                                                                                                                                                                                                                                                                                                                 ! Aao13785 Human polypeptide SEQ ID NO 276
                                                                                                                                                                                                                                                                                                                                                                                                        I Aao13576 Human polypeptide SEQ ID NO 274
```

KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK		27:	26:	25:	24 :	23:	22:	21:	20:	19:	18:	17:	16:	15:	ААМ1	274:	273:	AAU1	274:	273:	AAU1	57:	56:	55:
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK		KKKKR	KKKKK	KKKKK	RKKKK	RRKKK	RRRKK	RRRRK	RRRRR	GRRRR	RGRRR	RRGRR	RRRGR	RRRRG	411	VFAPR	QVFAP	804	VFAPR	QVFAP	79	KKKKK	KKKKK	KKKKK
3 3 4 118049 Human immunoglobulin polypeptide 14119 Peptide #553 encoded by probe for	æ														5383 len: 86			7611 len: 315	(K){20} KKKKKKKKKKKKKKKKKKKK		7016 len: 315	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK F
10 10		RRRR	RRRR	RRRR	KRRR	KKRRR	Aam14119 Peptide #553 encoded by	SGRSR	KGGRS	Aau18049 Human immunoglobulin	3GRSR	KGGRS	Aau17983 Human immunoglobulin	AGGGG	KAGGG	KKAGG								

KKKKK
KKKKK
KKKKK
XXXXX
! Aaml4961 Peptide
NKQTK
RNKQT
RRNKQ
RRRNK
RRRRN
RRRRR

(R,K){20}

RKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	48: RRRRR	47: RRRRR	46: ERRRR	45: KERRR	44: RKERR	43: GRKER	42: EGRKE	AAM15826	49: EEKKK	48: EEEKK	47: KEEEK	46: KKEEE	23: EEEEE	AAM15527	35: GRGRR	34: EGRGR	33: EEGRG	AAM15038	67: KXRKR	66: KKKRK	65: KKKKR	64: RKKKK	63: RRKKK	
115038 Peptide #1472 encoded by 115527 Peptide #1961 encoded by 115826 Peptide #2260 encoded by	(R,K){20} RRRRRRRRRRKRKRRRRRR	(R,K){20} RRRRRRRRRRRKRKRKRRRR						1939 len:						2276 len: 8				9082 len:					(R,K){20}	
be for for	KKKKK	RKKKK	RRKKK	RRRKK	RRRRK	RRRRR	RRRRR	Aam15826 Peptide #2260 encoded by probe	EEEEE	H	RKEEE	KRKEE	EEEKK	Peptide #1961 encoded by probe	GGGRR	RGGGR	RRGGG	Aam15038 Peptide #1472 encoded by probe			KK	KKK	XXXX ·	

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(K){20}
                                                                             (K){20}
                                                                                                                                                                               (K){20}
                                                                                                                                                                                                   (K) [20]
                                                                                                                                                                                                                                         (K) (20)
                                                                                                                                                                                                                                                              (K){20}
                                                                                                                                                                                                                                                                                 AAM16123 ck: 3607 len: 88
                                                                                                                                                                                                                                                                                                                                                                                                             (R,K){20}
S2: RERRE REFERENCE KKEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                (R,K)(20)

1: RERRER REREREREREREREREKKE KEKEEE
                                                                                                                                                                                                                                                                                                     (K){20}
                                                                                                                                                                                                                                                                                                                                                                       (R, K) [20]
54: RRRRR RRRRKKKKKKK EEEEE
                                                                                                                                                                                                                                                                                                                                                                                          (R,K){20}
S3: RRRRR RRRRRRKKKKKKKKKEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    50: RRRRR RRRRRRRRKKKKKRRRRRKK KKKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (R,K){20}
49: RERER REFEREREREKKERREREK KKKKK
                                                                                                                                                                                                                                                                                                                                                  ! Aam16123 Peptide #2557 encoded by probe
```

9: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	8: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	7: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	6: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	5: KKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	4: KKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	3: KK KKKKKKKKKKKKKKKK KKKKK	2: K KKKKKKKKKKKKKKK KKKKK	1: KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAM16691 ck: 3937 1en: 85   Aam16691 Peptide #3125 encoded by probe for (R,K)[20]	K KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK		(K){20}	67: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	66: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	65: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	64: KKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	63: KKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	62: KKKK KKKKKKKKKKKKKKKKKK KKKKK  (K)1201	61: KKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	60: KKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	59: KKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	58: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	57: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	56: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
(R.K){20} 40: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)[20] 39: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)[20] 38: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)[20] 37: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	36: KKKKK KKKKKKRKRKKKKKKKKKKKKKKKKKKKKKK	35: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	34: KKKKK KKKKKKRRKRKKKKKKKKKKKKKKKKKKKKK	-(R,K)(20)	32: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20}	(R,K)[20] 30: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)(20) 29: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	28: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	A): KRKK KRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK		26: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20}  (R,K){20}	(K)(20)  24: QKKKK KKKKKKKKKKKKKKKKKKK RKRKK	(K)(20) 23: KOKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	22: KKOKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	21: KKKOK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	1 (R,K)[20] (K)[20] 20: KKKKQ KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AAM17388 ck: 2686 len: 71   Aam17388 Peptide #3822 encoded by probe	11: KKKKK KKKKKKKKKKKKKKKKKKKK EBBEX	10: KKKKK KRKKKKKKKKKKKKKKKKKKKKKKKKKKKKK

56:	55:	54:	53:	52:	51:	50:	49:	48:	47:	46:	45:	44:	43:	ААМ	49:	48:	47:	46:	45:	44:	43:	42:	41:
RRRRR	ERRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	GRRRR	RGRRR	RRGRR	ERRGR	RERRG	ААМ18532	RKRKK	KRKRK		KKKRK	45: KKKKR	KKKKK	KKKKK	KKKKK	KKKKK
(R)(20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) RRRRRKRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R,K){20} (R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 1560 len: 88	(K) [20] KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKRKR KKKKKKKKKKKKKKKKKK KKSAH	(R,K){20}	(R,K)(20)	RKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20}	(R,K){20}	(R,K){20} KKKRKRKKKKKKKKKKKKKK KKKKK
RRERR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRKRR	RRRRR	RRRRR	RRRRR	RRRRR	! Aam18532 Peptide #4966 encoded by probe for	SAH	KSAH	KKSAH	KKKSA	KKKKS	KKKKK	KKKKK	XXXXX	KKKKK
2	2	L.	L	1	<b>1</b>	1	<u>,,</u>			ني ،	<b>1</b>	Þ				ы	Ð	6	5	σ,	<b>U</b> 1	4.00	

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21: RRRRK KKKKKRKKKKKKKKKKRRRR RRRRR
                                                                                                                                                                                                      (R,K)[20]
20: RRRRR KKKKKKKKKKKKKKKKKKKRR RRRRR
                                                                  (R,K){20}

19: GRRRR RKKKKKKKKKKKKKKKKKRR RRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (R){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (R){20}
                                                                                                   (R,K){20}
18: RGRRR RRKKKKKKKKKKKKKKKKKKKR RRRRR
                                                                                                                                   (R,K){20}
17: RRGRR RRRKKKKKKKKKKKKKKKKKK RRRRR
                                                                                                                                                                     AAM26526 ck: 5383 len: 86
                                                                                                                                                                                                                                                                                    20: KPMRK RRRKKKRRKKKRKKKRRKK LTTTT
                                                                                                                                                                                                                                                                                                                    (R,K){20}
19: FKPMR KRRRKKKRRKKKRRKKKLTTT
                                                                                                                                                                                                                                                                                                                                                    (R,K){20}
(R,K){20}
18: LFKPM RKRRRKKKRRRKKRRKKKRRR KKLTT
                                                                                                                                                                                                                                                                                                                                                                                                   AAM21941 ck: 4895 len: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM20089 ck: 8343 len: 66 ! Aam20089 Peptide #6523 encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9: REKKK KRKKKKKKKKKKKKKKKKKK NKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (R,K){20}
                                                                                                                                                                                                                                                 1 Aam26526 Peptide #563 encoded by probe f
                                                                                                                                                                                                                                                                                                                                                                                                ! Aam21941 Peptide #8375 encoded by probe
```

45: RI	44: RI	43: RI	42: R	41: K	40: K	39: K	38: K	37: R	36: K	35: K	34: K	33: K	32: K	31: R	30: K	29: K	28: K	27 : K	26: K	25: K	24: R	23: R	22: R
RRRRR I	RRRRR	RRRRR I	RRRRR 1	KRRRR	KKRRR	KKKRR	KKKKR	RKKKK	KRKKK	KKRKK	KKKRK	KKKKR	KKKKK	RKKKK	KRKKK	KKRKK	KKKRK	KKKKR	KKKKK	KKKKK	RKKKK	RRKKK	RRRKK
(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20}	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R,K){20} KRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K){20} KKRRRRRRRRRRRRRRRRRRRR	(R,K){20} KKKRRRRRRRRRRRRRRRRR	(R,K){20} KKKKRRRRRRRRRRRRRRRR	(R,K){20} RKKKKRRRRRRRRRRRRRRR	(R,K){20} KRKKKKRRRRRRRRRRRRRRR	(R,K){20} KKRKKKKRRRRRRRRRRRRR	(R,K){20} KKKRKKKKRRRRRRRRRRRR	(R,K){20} KKKKRKKKKRRRRRRRRRR	(R,K){20} KKKKKRKKKKRRRRRRRRR	(R,K){20} RKKKKKRKKKKRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K)(20) KRKKKKKRKKKKRRRRRRRR	(R,K){20} KKRKKKKRKKKKRRRRRRR	(R,K){20} KKKRKKKKKKKKKKKRRRRRR	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
NKQTK	RNKQT	RRNKQ	RRRNK	RRRRN	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR

```
(R,K){20}
(R,K){20}
23: EEEEE KKKKKKRKKKKKKKKKKKK EEEKK
                                                                                                                                                                                                                                                                                                              AAM28336 ck: 1939 len: 130 ! Aam28336 Peptide #2373 encoded by probe
                                                         49: EEKKK KKKKKKKKKKKKKKKKKKK EEEEE
                                                                                       48: EEEKK KKKKKKKKKKKKKKKKKKK KEEEE
                                                                                                                    (K)(20)
47: KEEEK KKKKKKKKKKKKKKKKKKKK RKEEE
                                                                                                                                                  (K){20}
                                                                                                                                                                                                                                                                                                                                                                                    (R,K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35: GRGRR RRRRKKRRKKRRKKRRK GGGRR
                                                                                                                                                                                                                                                                                 (R,K)[20]
34: EGRGR RRRRRRKRRKRRKRR RGGGR
                                                                                                                                                                                                                                                                                                                                                    AAM27479 ck: 9082 len: 167 ! Aam27479 Peptide #1516 encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM27395 ck: 1334 len: 86
                                                                                                                                                                                                                       AAM28016 ck: 2276 len: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (R,K) [20]
(R,K) [20]
                                                                                                                                                                                                                     ! Aam28016 Peptide #2053 encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ! Aam27395 Peptide #1432 encoded by probe
```

42: ECRKE RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR		48:	47:	46:	45:	44:	43:	42:	41:	40:	39:	AAM:	54:	53:	52:	51:	50:	49:	48:	47:	46:	45:	44:	43:	42:
RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR		KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	EKKKK	REKKK	KREKK	RKREK	ERKRE	28616	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	ERRRR	KERRR	RKERR	GRKER	
28616 Peptide #2653 encoded by probe	(K){20}				(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK			(K) {20}	(K) {20}	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	3607 len:	(R,K){20} RRRRKRKRRRRRRKKKKKK	(R,K){20} RRRRRKRKRRRRRRKKKKK	(R,K){20} RRRRRRKRKRKRRRRRKKKK	(R,K){20} RRRRRRRKRKRRRRRKKK	(R,K){20} RRRRRRRRKRKRRRRRKK		(R,K){20} RRRRRRRRRRKRKRKRRRRR	(R,K){20} RRRRRRRRRRRKRKRRRRR	(R,K){20} RRRRRRRRRRRRRKRKRRRR	(R,K){20} RRRRRRRRRRRRRKRKRRR	(R,K){20} RRRRRRRRRRRRRRKRKRK	(R,K){20} RRRRRRRRRRRRRRRRKRKR	
·	_	KKKKK	KKKKK	KKKKK		KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	Aam28616 Peptide #2653 encoded by probe	EEEEE	KEEGE	KKEEE	KKKEE	KKKKE	KKKKK	KKKKK	RKKKK	RRKKK	RRRKK	RRRRK	RRRRR	RRRRR

ب

	<u>ې</u>	1.	AAM:	69:	68:	67 :	66:	65:	64:	63:	62:	61:	60:	59:	58 :	57:	56:	55:	54:	53:	52:	51:	50:	49:
	*		ААМ29178	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
(K)[20]	(K){20} KKKKKKKKKKKKKKKKK KKKKK	(R,K)[20] (K)[20] KKKKKKKKKKKKKKKKK KKKKK	ck: 3937 len: 85   Aam29178 Peptide #3215 encoded by probe	(K){20} KKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKK K	(K)(20)	(K){20} KKKKKKKKKKKKKKKKK KKK	(K)[20] KXKKKKKKKKKKKKKKKK KKKK	(K)(20) KKKKKKKKKKKKKKKKKK KKKKK	(K)(20) KKKKKKKKKKKKKKKKK KKKKK	(K){20} KKKKKKKKKKKKKKKKK KKKKK	(K)[20] KRKKKKKKKKKKKKKKKK KKKKK	KKKKKKKKKKKKKKKKK KKKKK	KKKKKKKKKKKKKKKK KKKKK	(K)(20) KKKKKKKKKKKKKKKKKK KKKKK	(K){20} KKKKKKKKKKKKKKKKKK KKKKK	(K)[20] KKKKKKKKKKKKKKKKK KKKKK	(K)[20] KKKKKKKKKKKKKKKKK KKKKK	(K)[20] KKKKKKKKKKKKKKKKK KKKKK	(K)[20] KKKKKKKKKKKKKKKKK KKKKK	(K){20} KKKKKKKKKKKKKKKKK KKKKK	(K){20}	KKKKKKKKKKKKKKKKK KKKKK	KKKKKKKKKKKKKKKKK KKKKK

	56:	55:	54.:	53:	52:	51:	50:	49:	48:	47:	46:	45:	4 4 	ֆ 3:	AAM	11:	10:	9:	8	7:	6:	5.	4	ω 
	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	GRRRR	RGRRR	RRGRR	ERRGR	RERRG	ААМ30989	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKK	KKK	XX
(R) {20}	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)[20] RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R)(20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R){20} RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	(R,K)(20) (R)(20) RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	ck: 1560 len: 88	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) { 20 }	(K) (20) KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K) {20}	(K){20} KKKKKKKKKKKKKKKKKKKK	KKKKKKKKKKKKKKKKKK KKKKK
	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	RRRRR	Aam30989 Peptide #5026 encoded by probe for	EEEEX	KEEEE	KKEED	KKKEE	KKKKE	KKKKK	KKKKK	KKKKK	KKKKK
	-	•							ы					1			L.							

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(R,K){20}
(R,K){20}
16: KERKT KKRKRKRRRKKRRRKKRR R
                                                                                          AAM37018 ck: 4228 len: 24
                                                                                                                                                AAM36456 ck: 2394 len: 57 ! Aam36456 Peptide #10493 encoded by prob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (R){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (R){20}
S9: RERER RERERERERERERERERERERE
                                                                                                                                                                                                                                                                                                                                                                                         AAM33953 ck: 8343 len: 66 ! Aam33953 Peptide #7990 encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                      (R,K)[20]
17: ERKTK KRKRKRRRKKRRRKKRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (R){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM31173 ck: 2324 len: 36 ! Aam31173 Peptide #5210 encoded by probe
                                                                                                                                                                                                                                                                                                                                                      (R,K)(20)
(R,K)(20)
(R,K)(20)
                                                                                                                                                                                                                                                                     (R,K){20}
(R,K){20}
RRRRRRRKKKKRRRRRRRRR RKRT
                                   ! Aam37018 Peptide #11055 encoded by probe
```

(R,K){20}

31:	30:	29:	28:	27:	26:	25:	24:	23:	22:	21:	20:	19:	18:	17:	16:	15:	14:-	13:	12:	ААМЗ	<u>4</u>	ա 	2:
KRKKK	RKRKK	KRKRK	RKRKR	KRKRK	RKRKR	KRKRK	KKRKR	KKKRK	KKKKR	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	NKKKK	KNKKK	KKNKK	KKKNK	KKKKN	ААМ37794	RRR	RR	R
(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(R,K){20} RKKKKKKKKKKKKKKKKKKK	(R,K){20}	RKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20} KRKRKKKKKKKKKKKKKKKK	(R, K) {20} RKRKRKKKKKKKKKKKKKKK	(R,K){20} KRKRKRKKKKKKKKKKKKKK	(R, K) (20)	(R, K) {20} KRKRKRKRKKKKKKKKKKK	(R,K)(20)	(R,K){20} KKKRKRKRKRKKKKKKKKKK	(R,K){20}	(R, K) {20} KKKKKRKRKRKKKKKKKKK	(R, K) {20} KKKKKKRKRKRKRKKKKKKKK	(R, K) {20} KKKKKKKRKRKRKRKKKKKK	(R, K){20} KKKKKKKKRKRKRKRKKKKK	(R,K){20} (R,K){20}	ck: 3301 len: 52	(R,K){20} RRRRKKKKRRRRRRRRRKR	(R,K){20} RRRRRKKKKRRRRRRRRRK	RRRRRKKKKRRRRRRRRRR
AF .	KAF	KKAF	KKKAF	KKKKA	XXXX	XXXX	XXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	! Aam37794 Peptide #11831 encoded by probe fo	-3	RT	KRT

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(K){20}
               (K) (20)
                                                                                                                                                                                                                                                                                                                                                                (R,K){20}
(R,K){20}
18: LFKPM RKRRRKKKRRRKKKKKKKRRR KKLTT
                                                                               (K){20}
                                                                                              (K){20}
                                                                                                                                                                                                                                                                                                                                                                                      AAM38273 ck: 4895 len: 51 ! Aam38273 Peptide #12310 encoded by probe
                                                                                                                                                                                              AAU04283 ck: 8137 len: 45
                                                                                                                                                                                                                                                                                                                                  (R,K){20}

KPMRK RRRKKKRRKKKRKKKRRKK LTTTT
                                                                                                                                                                                                                                                                                                                                                 19: FKPMR KRRRKKKRRRKKRKKKRRRK KLTTT
                                                                                                                                                                                                              5:
                                                                                                                                                                                                                                             ! Aau04283 Trimeric fusogenic peptide #2 u
```

38: KKKKK	37: KKKKK	36: KKKKK	35: KKKKK	34: KKKKK	33: KKKKK	32: KKKKK	31: KKKKK	30: KKKKK	29: KKKK	28: KKKKK	27: KKKKK	26: KKKKK	25: KKKKK	24: KKKKK	23: KKKKK	22: AKKKK	21: KAKKK	20: YKAKK	19: РҮКАК	18: АРҮКА	AAU04285	24: KKKKK	23: KKKKK
(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20}	(K)(20) K KKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20}	(K){20} K KKKKKKKKKKKKKKKKKKK	(K){20} K KKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} K KKKKKKKKKKKKKKKKKK	(K){20} K KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20} K KKKKKKKKKKKKKKKKKK	(K){20}	(K){20}	(K){20} K KKKKKKKKKKKKKKKKKKK	(K){20} K KKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} A KKKKKKKKKKKKKKKKKKKK	ck: 4361 len: 59	(K){20} K KKKKKKKKKKKKKKKKKKK	(K){20} K KKKKKKKKKKKKKKKKKKK
WK	KWK	KKWK	KKKWK	KKKKW	KKKKK	XXXXX	XXXXX	KKKKK	KKKKK	XXXXX	KKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	! Aau04285 Nuclear ligand #2 used in nucleic	WK	KWK
																						1	

```
(K){20}
                                          (K){20}
                                                  AAU04287 ck: 4925 len: 100 ! Aau04287 Poly-L-Lysine used in nucleic i
                                                                                                                   2:
                                                                                                                                                                                      ::
                                                                                                                            5:
                                                                                                                                                    (K){20}
                                                                                                                                                            (K)[20]
                                                                                                                                                                     (K)[20]
KK KKKKKKKKKKKKKKKKKKKK KKKK
                                                                                                                                                                             (R,K){20}
(K){20}
```

	47:	46:	45:	44:	43:	42:	41:	40:	39:	38:	37:	36:	35:	34:	ω ω	32:	31:	30:	29:	28:	27:	26:	25:	24:
	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	XXXXX	KKKKK
(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K)[20] KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K)[20] KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K)(20)	(K) {20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K)(20) KKKKKKKKKKKKKKKKKKKKK
	KKKKK	KKKKK	XXXXX	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK

72:	71:	70:	69:	68:	67:	66:	65:	64:	63:	62:	61:	60:	59:	58:	57:	56:	55:	54:	53:	52:	51:	50:	49:	48:
KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK	KKKKK
(K){20} KKKKKKKKKKKKKKKKKKKKK KKKK	(K){20} KKKKKKKKKKKKKKKKKKK KKKKK	(K){20}	(K){20}	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKK KKKK	(K){20} KKKKKKKKKKKKKKKKKKKK KKKK	(K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20}	KKKKKKKKKKKKKKKKKK KKKKK													

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28: KKKRK KKKKRKKKKRRRRRRRRRRR RRRRR
                                  27: KKKKR KKKKKKKKKRRRRRRRRR RRRRR
                                                                                                                                                                              23: RRKKK KKKRKKKKKKKKKKRRRRR RRRRR
                                                                    (R,K)(20)
26: KKKKK RKKKKKKKKKKKRRRRRRRRR RRRRR
                                                                                                        25: KKKKK KRKKKKKKKKKKRRRRRRR RRRRR
                                                                                                                                          (R,K)[20]
24: RKKKK KKRKKKKKKKKKKKRRRRRR RRRRR
                                                                                                                                                                                                                     22:
                                                                                                                                                                                                                                                     21: RRRRK KKKKKRKKKKKRKKKKRRRR RRRRR
                                                                                                                                                                                                                                                                                         (R, K) [20]

ORRER KKKKKKKKKKKKKKKKKKRR RERERE
                                                                                                                                                                                                                                                                                                                           (R,K){20}

GRRRR RKKKKKKKKKKKKKKKKKKRR RRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80: KKKKK KKKKKKKKKKKKKKKKK K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18: RGRRR RRKKKKKKKKKKKKKKKKKK RRRRR
                                                                                                                                                                                                                                                                                                                                                                                                   (R,K){20}
17: RRGRR RRRKKKKKKKKKKKKKKKKKK RRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                     (R,K)(20)

(R,K)(20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM01857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (K){20}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75: KKKKK KKKKKKKKKKKKKKKKK KKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (R,K)(20)
RRRKK KKKKRKKKKKKKKKRRRRR RRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ck: 5383 len: 86
                                                                                                                                                                                                                                                                                                                                                                             (R,K)[20]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ! Aam01857 Peptide #539 encoded by probe for
```

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60:
                                                                       (R){20}
                                                                                                                                                                                              (R){20}
                                                                                                                                                                                                                           (R){20}
                                                                                            AAM02687
                                                                                                                                                                                                                                         35: KKRKK KKRRRRRRRRRRRRRRRRRR RRRRR
                                                                                                                                                                                                                                                                      32: KKKKK RKKKKRRRRRRRRRRRRRRRR RRRRR
                                                                                                                                                                                                                                                                                                                31: RKKKK KRKKKKRRRRRRRRRRRRRR RRRRR
                                                                                                                                                                                                                                                                                                                              30: KRKKK KKRKKKKRRRRRRRRRRRRR RRRRR
                                                                                                                                                                                                                                                                                                                                            29: KKRKK KKKRKKKKRRRRRRRRRRRR RRRRR
                                          ck: 1334 len: 86
                                                                                         ! Aam02687 Peptide #1369 encoded by probe
```

55: KKKKK KKKKKKKKKKKKKKKKKKKK KKKKK	in the second
	(R,K)(20)
(K){2O}	(R,K)(20) 47: RRRRR RRRRRRRRKRKRKRRRRR RKKKK
(x){20}	46: ERRRE RRRERRERRERRERRERRERRERRERRERRERR
52: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20} 45: KERRR RRRRRRRRRRRRRRRRRRRRRRRRKK
• (x)[20] 51: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20} 44: RKERR RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
50: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20} 43: GRKER RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
(K)(20) 49: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)(20) 42: EGRKE RRRRRRRRRRRRRRRKRK RRRRR
(K)(20)  48: KKKKK KKKKKKKKKKKKKKKKK KKKKK	AAMU3564 CK: 1939 len: 130 ! Aam03564 Peptide #2246 encoded by probe for (R.K)[20]
(K)(20) 47: KKKKK KKKKKKKKKKKKKKKKK KKKKK	X XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
(K)(20) 46: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K)[20]
45: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(R,K){20}
44: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	47: KEEEK KKKKKKKKKKKKKKKKK RKEEE
43: EKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K)(20)  (K)(20)  (K)(20)
REKKK	(R,K)(20) (R,K)(20) 23: EEEEE KKKKKKKKKKKKKKKKK EEEKK
(K){20} 41: KREKK KKKKKKKKKKKKKKKKKKK KKKKK	AAM03278 ck: 2276 len: 89 ! Aam03278 Peptide #1960 encoded by probe for
(K){20} 40: RKREK KKKKKKKKKKKKKKKKKK KKKKK	(R,K)(20) 35: GRGRR RRRRKRRRKRRKRRKRRR GGGRR
39: ERKRE KKKKKKKKKKKKKKKKKKK KKKKK	(R,K)(20) 34: UGRGR RRRRRKRRKRRKRRKRR RGGGR
AAM03848 ck: 3607 len: 88	(R,K)(20) (R,K)(20) (R,K)(20)
(R,K){20} 54: RRRRR RRRRKKKKRRRRRKKKKKKK EEEEE	AAM02768 ck: 9082 len: 167 ! Aam02768 Peptide #1450 encoded by probe for
(R,K)(20) 53: RRRRR RRRRRKKKRRRRRKKKKK KEEEE	(X)[20] 67: KKRKR KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
(R,K)[20] 52: RRRRR RRRRRRKKKKRRRRRKKKK KKEEE	(R.K){20} 66: KKKRK RKKKKKKKKKKKKKKK K
(R,K){20} 51: RRRRR RRRRRRRKKKRRRRRKKK KKKEE	(R.K){20} 65: KKKKR KRKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
(R,K)(20) 50: RRRRR RRRRRRRKKKKRRRRRKK KKKKE	(R,K){20} 64: RKKKK RKRKKKKKKKKKKKKKKKKKKKKKKKKKKKK
(R,K)[20] 49: RRRRR RRRRRRRRRKRKRKRRRRK KKKKK	(R.K){20} 63: RRKKK KRKKKKKKKKKKKKKKKKKKKKKKKKKKKKK

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(K){20}
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RR RRRRRRRRKRKRKRRRRKK KKKKE
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(K){20}
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9: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKEEE
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                                                                                                                           47:
                                                                                                                                  (K){20}
                                                                                                                                                                                      AAM06100 ck: 1560 len: 88
1 Aam06100 Peptide #4782 encoded by probe
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AAG73687 ck: 3063 len: 29

! Aag73687 Human colon cancer antigen pro1

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(K)[20]	(K){20} KKKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKK	(K) (20) KKKKKKKKKKKKKKKKKKKK	(K)[20]	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(R,K)(20) (K)(20) KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 3:	(K){20}	(K){20}	(K){20}	(K){20}	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK	(K){20}	(R,K)(20) (K)(20) KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ck: 783	(K){20} KKKKKKKKKKKKKKKKKKK	(R,K){20} (K){20} KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
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80: KKKKK KKKKKKKKKKKKKKKKKKK XGXPF
                            AAG74218 ck: 8659 len: 104 | Aag74218 Human colon cancer antigen prot
                                                                                                          (K){20}
22: VRKKK KKKKKKKKKKKKKKKKKK GG
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(K) (20)	(R,K)(20)	AAG74793 ck: 8497 len: 152 ! Aag74793 Human colon cancer antigen protein	16: KKKKK KKKKKKKKKKKKKKKKK GXPF	5: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	44: KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKK	43: KKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK					19. BOKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	38: CROKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	37: QCRQK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	36: LQCRQ KKKKKKKKKKKKKKKKKK KKKKK		AAG74650 ck: 1596 len: 69 ! Aag74650 Human colon cancer antigen protein	(K)[20] 17: KKKKK KKKKKKKKKKKKKKK GXPX	(K)(20) 16: KKKKK KKKKKKKKKKKKKKKK KGXPX	15: KKKKK KKKKKKKKKKKKKKKK KKGXP	14: KKKKK KKKKKKKKKKKKKKKK KKKGX	13: YKKKK KKKKKKKKKKKKKKKKK KKKKG	12: LYKKK KKKKKKKKKKKKKKKKK KKKKK	11: LLYKK KKKKKKKKKKKKKKKKK KKKKK	10: LLLYK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	9: CLLLY KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK		AAG74527 ck: 2664 len: 40   Aag74527 Himan colon cancer anticen protein
. 1 (R, F	AAG75215 ck:	76: KKKKK KKK	(K	75. KEKKK KKK 15. KEKKK KKK 15. KEKKK KKK 15. KEKKK 15. KEKK 15. KEKK 1	74: KKKKK KKK	73: KKKKK KKKI	(K) 72: KKKKK KKK	71: KKKKK KKKI	70: kkkkk kkk	69: KKKKK KKKI	68: KKKKK KKK	67: XXXXX XXX			65: KKKKK KKK	64: KKKKK KKK	63: KKKKK KKK	62: KKKK KKK	61: EKKKK KKK	60: KEKKK KKK	59: RKEKK KKK	58: LRKEK KKK	57: NLRKE KKK	1 (R,		173. SUTTON KKK	122: SSHTQ KKK
(R,K)[20]	3913 len: 155 ! Aag75	KKKKKKKKKKKKKKKK XGG	(K) {20}	(20)	){20} KKKKKKKKKKKKKKKKKK KKXGG	),{20} KKKKKKKKKKKKKKKKKK KKKXG	XKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(){20}	(K){20}	(K){20} KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	KKKKKKKKKKKKKKKK KKKKK	(K) {20}	(K){20}	(K){20}	(K){20} KKKKK KKKKKKKKKKKKKKKKK KKKKK	(K)(20) KKKKK KKKKKKKKKKKKKKKKKK KKKKK	(K){20} KKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} EKKKK KKKKKKKKKKKKKKKKKK KKKKK	(K)(20) KEKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	(K){20} RKEKK KKKKKKKKKKKKKKKKKKK KKKK	(K){20} LRXEK KKKKKKKKKKKKKKKKKKKK KKKKK	(K){20} KKKKKKKKKKKKKKKKKKKK KKKK	K)[20]	1215 122 00 1 227	(K)[20]	122: SSHTQ KKKKKKKKKKKKKKKKKKKK KXKKK

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AAG75215 ck: 3913 len: 155 ! Aag75215 Human colon cancer antigen pro
                                       (K){20}
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                         (K){20}
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(K) [20]
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(K){20}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE01796 ck: 4416 len: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (K){20}
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(K){20}
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AAB45848 ck: 4361 len: 59

! Aab45848 Nucleic acid transporter system

ω 	2:	1:	AAB,	38:	37:	36:	35:	34:	33:	32:	31:	30:	29:	28:	27:	26:	25:	24:	23:	22:	21:	20:	19:
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                            ! Abb44830 Human protective sequence CNI-007
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Total finds:
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EMBL, Release 7.0, Released on 28Apr2002, Formatted on 2May2002
                                                                                          29: KKKKK KKKKKKKKKKKKKKKKKK GR
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